

**Differential Gene Expression in Explanted Human Retinal Pigment Epithelial Cells
24-hours Post-Exposure to 532 nm, 3.0 ns Pulsed Laser Light and 1064 nm, 170 ps
Pulsed Laser Light 12-hours Post-Exposure: Results Compendium**

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This article, "Differential Gene Expression in Explanted Human Retinal Pigment Epithelial Cells 12-hours Post-Exposure to 532 nm, 3.0 ns Pulsed Laser Light and 1064 nm, 170 ps Pulsed Laser Light 12-hours Post-Exposure: Results Compendium," is presented as a competent treatment of the subject, worthy of publication. The United States Air Force Academy vouches for the quality of the research, without necessarily endorsing the opinions and conclusions of the authors. Therefore, the views expressed in this article are those of the authors and do not reflect the official policy or position of the United States Air Force, Department of Defense, or the US Government.

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ROBERT S. FREDELL, Lt Col, USAF
Director of Faculty Research

Date

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Differential Gene Expression in Explanted Human Retinal Pigment Epithelial Cells 24 hours Post-Exposure to 532 nm, 3.0 ns Pulsed Laser-Light and 1064 nm, 170 ps Pulsed Laser-Light 12 hours Post-Exposure: Results Compendium

ABSTRACT

The use of laser light for military and commercial applications has sharply increased the likelihood of personnel exposure to laser light during operations. The increased potential for human exposure highlights the fact that there is paucity of basic science at the cell and molecular level concerning the effects of laser exposure of human cells. Current safety standards are largely extrapolations of exposure limits using a minimal visible lesion endpoint in the Rhesus monkey retinal model. A non-animal model for assessing laser-light damage to tissue, particularly human, is quite desirable for obvious scientific, political, and fiduciary reasons. We assessed the sublethal insult to human retinal pigment epithelial cells using a cadaver organ donor explant system for genes differentially expressed 12 and 24 hours post-exposure using gene expression microarray technology (gene chip). It appears that pulses of laser light are sensed and markedly alter gene expression. The two experiments presented herein are intended to add to the database of laser-tissue interaction at the molecular level using gene expression profiling as the assessment endpoint. This investigative approach also showcases a global methodology for characterizing environmental stressors on a living system via genetic profiling and hallmarks the use of human explants as an experimental model for assessing laser-induced bioeffects at the cell and molecular level. Additionally, we offer 3 conceptual cartoons outlining our vision for the future progress of laser bioeffects research, metabonomic risk assessment modeling and knowledge building from laser bioeffects data.

BACKGROUND

In the interest of brevity the reader is referred to USAFA-TR 2004-01 for the background.

MATERIALS AND METHODS

Explant procurement and processing: General overview

Tissues were received as a tissue donor gift through the Rocky Mountain Lion's Eye Bank who accomplishes all of the donor consent paperwork. Posterior globes of both eyes were harvested 8 hours post time of death and put into a 50 ml vial with approx. 25 ml of buffered saline. The tissue was transported directly to tissue culture lab where the vitreous humor and retina were mechanically removed. Then the RPE still attached to the sclera were cut into 3-5 mm square pieces. The pieces were then placed into 96 well microtiter plates (1 per well) with 150 microliters (ul) of the media (DME/F12 with 10% FBS plus antibiotics) and cultured at 37 degrees C in 5% CO2 until re-plated for

exposure. In a fresh 96 well plate the pieces were placed RPE side up centered in the well, in 50 ul media (just covers the explant) to be exposed. Explants were kept at 37 degrees until they were transported in a pre-warmed insulated box to the laser lab and exposed at room temperature in the plates on an X-Y translation stage one well at a time as quickly as possible to minimize temperature fluctuations then returned to the incubator after stereoscopic examination and the additional 100 ul of warm media. At the desired time post exposure, RPE was mechanically removed from the sclera and collected in microcentrifuge tubes, labeled and frozen at -65 degrees C. Samples were shipped frozen to the vendor with approx. 10 lbs of dry ice via overnight delivery. We accepted donors age 65 years or younger, either sex, with no mitigating ocular or retinal pathology such as glaucoma, diabetic retinopathy, retinitis pigmentosa, etc.

This report provides the results of two gene expression experiments. The first was a 532 nm, nanosecond pulse width exposure designated as N2. The second was a 1064 nm, picosecond pulse width exposure designated as P4.

Donor:

The RPE tissue donor for N2 was a 65 year old Caucasian, blue eyed, male that died of cancer. The RPE tissue donor for P4 was a 41 year old Caucasian, blue eyed, female that died of cancer. No ocular pathologies were noted.

Explant preparation: See USAFA-TR-2004-01

Laser: Equipment Used for N2

| | |
|--------------------|----------------------------------|
| Laser (Nd:YAG) | Coherent Infinity XPO Laser |
| Power Meter | Scientech Power Meter model S310 |
| Detector Head | Scientech model PHDX50 |
| Shutter | nmLaser model LS055S3W8 |
| Shutter Controller | nmLaser model CX2450 |
| Velmex XY Stage | model NF90-2 |

Laser: Equipment Used for P4

| | |
|--------------------|---|
| Laser (Nd:YAG) | EKSPLA, model SL312T, serial number 017 |
| Power Meter | Moletron OM4001 power meter, serial number 136C |
| Detector Head | J50 Detector Head, with diffuser, serial number 1518B |
| Shutter | nmLaser model LS055S3W8 |
| Shutter Controller | nmLaser model CX2450 |
| Velmex XY Stage | model NF90-2 |

In both exposures the pulse energy was determined by placing a power meter on the x-y translation stage (the site of target exposure) and dividing the measured average power by

the pulse repetition rate. This method was considered adequate since pulse-to-pulse energy typically varied less than 10%. The beam profile is a "top hat" with less than 5% variation across the wave front.

Laser-light exposure:

For procedures see USAFA-TR-2004-01. In the table below are the exposure parameters for the experiments reported herein.

| Treatment | N2 | P4 |
|-----------------------------------|--------------------|--------------------|
| Wavelength (nm) | 532 | 1064 |
| Average Power (mW) | 508 | 1150 |
| Pulse Energy (mJ) | 50.8 \pm 1.2 | 115 \pm 5 |
| Pulse Length (FWHM) | 3.0 ns | 170 ps |
| Total Incident Energy (mJ) | 3251 | 3220 |
| Peak Power (W) | 1.69 $\times 10^7$ | 6.76 $\times 10^8$ |
| Fluence (mJ/cm ²) | 108 | 244 |
| Exposure Time (sec) | 6.4 | 2.8 |
| Laser Repetition Rate (Hz) | 10 | 10 |
| Beam Diameter (1/e ²) | 6 mm | 6 mm |
| Irradiance (kW/m ²) | 18.0 | 40.7 |

Total incident energy (TIE) is defined as the amount of laser-light energy that was delivered to the 6 mm well containing the RPE explants. Abbreviations: nm-nanometer; m-meter, mm-millimeter, ns-nanosecond; mJ-milliJoule; mW-milliWatt; FWHM-Full Width Half Max; Hz-Hertz; sec-second; W-watt; e-natural log.

Laser exposure of Human RPE Explants

The Nd:YAG laser light exposure regimen was based on empirical data (not shown) that established cell viability after a range of laser exposures. The exposure described above for treatment N2 was calculated to be 1.8 kJ/m² which is about 10% of the MVL value and approximately 65% above the MPE for the pulse width and wavelength considered (Sloney and Wolbarsht, 1980 and ANZI Z136.1-2000 Table 5a). The exposure described above for treatment P4 was calculated to be 4.1 kJ/m² which is about 16% of the MVL value and approximately 20% above the MPE for the pulse width and wavelength considered (Sloney and Wolbarsht, 1980 and ANZI Z136.1-2000 Table 5a)

In experiment N2 the cells were exposed to either 1) sham exposed to no laser-light (beam blocked upstream), or 2) 64 pulses of 532 nm visible laser-light. Each pulse containing 50.8 mJ \pm 1.2 mJ (on average) of energy was delivered to a microtiter plate well 6 mm in diameter containing 50 microliters of medium. In experiment P4 the cells were exposed to either 1) sham exposed to no laser-light (beam blocked upstream), or 2) 28 pulses of 1064 nm visible laser-light. Each pulse containing 115.5 mJ \pm 5 mJ (on

average) of energy was delivered to a microtiter plate well 6 mm in diameter containing 50 microliters of medium. See Figure 2 in USAFA-TR-2004-01 for a general overview of the experimental procedures.

Exposed RPE collection

Sample N2 was harvested 24 hours post-exposure for gene chip analysis; while sample P4 was harvested at 12 hours post-exposure. A "C" beginning the sample designation (i.e. CP4 or CN2) indicates the control sample for comparison. The "HX" designation indicates the use of human explanted tissue as the experimental model. See USAFA-TR-2004-01 for further procedural details.

Oligonucleotide Microarray Description Protocol and Analysis:

See USAFA-TR-2004-01.

For a complete listing of sequence sources and human array design the reader should visit Affymetrix's website at www.affymetrix.com, Technical Note: Array Design for the GeneChip Human Genome U133 Set.

RESULTS

The results (Appendix A and B) of a gene expression microarray are expressed in fold change in expression for one gene in the control versus the experimental samples. For example, if gene YFG is expressed four times greater in the treated cells than in the sham exposed controls, it would show a fold change of positive four (4) in Appendix A that functionally means that gene YFG mRNA was found in 4 times greater concentration in the treated cells than in the controls. Thus, we conclude that the treatment induced the genetic expression of gene YFG four times greater in the experimentally treated cells than in the shame treated cells, presumably in response as the biological effect of the treatment. Conversely, if the YFG mRNA is 4 fold less in the experimental sample than in the control then a value of -4.0 fold is calculated. The assignment of the plus or minus designations on Appendix A is a function of the algorithm in the software used to calculate the fold change. In the context of understanding the significance of fold change or fold induction of a gene, the analysis software calculates a 95% confidence level of fold change for each experiment. For this set of hybridizations labeled N2 and P4 the confidence was calculated to be +/- 1.2 for both.

Appendices A and B presents the most pertinent genes (at or above the absolute value for significance) listed in rank ordered by absolute fold change minus to plus at or above the significance value. To help clarify the interpretation of this appendix the following heading explanations are offered. Probe set: the listed name of the gene being probed. Control probe sets have been deleted from the data set in Appendix A. All signals in Appendix A have passed the quality control standards established by the manufacturer. The internal controls are used by Affymetrix to calibrate the array and as quality control

elements. Control signal: the balanced (adjusted for background) signal strength for the control sample. Exptl Signal: the balanced (adjusted for background) signal strength for the experimental sample. Control vs Exptl Fold Change: the fold change based on the comparative signal strength of the control RPE sample as compared to the experimental. **This is the fold change value that is used as the endpoint value, and for further analysis in the interpretation of the differential gene expression microarray results for the designated genetic elements listed under "Probe set."** Description: a brief description of the gene or EST that is represented in the probe set. The appendix obviously contains only a portion of the total number of elements probed and only those whose absolute fold change was at least at the minimum significance level or higher that has been calculated to be at or above the statistical significance of 95%.

For experiment N2 a quick survey of the Fold Change (Figure 1), Variable Bin Histogram (Figure 2) and Differential Expression Scatter Plot (Figure 3) (internal controls are not in the graph data set) and Appendix A yields the observation that RPE mRNA was above 1.2 absolute fold change in 146 of the approximately 22, 000 (approximately 0.7%) probe elements on the GEM. Of those 77 (0.4% of the total possible elements and 52.7% of the significantly expressed elements) were up-regulated. The number of genes whose expression was down regulated was markedly less. 68 (0.3% of the total possible elements and 46.6% of the significantly expressed elements) genes were down-regulated at or above significant levels. In summary, the number of significant changes in gene expression was approximately equal in the up-regulated direction versus down-regulated direction, but the greatest magnitude of change for single genes was up-regulation with over two times greater fold change.

For experiment P4 a quick survey of the Differential Expression Scatter Plot (Figure 4) (internal controls are not in the graph data set) and Appendix B yields the observation that RPE mRNA was above 1.2 absolute fold change in 408 of the approximately 22, 000 (approximately 1.9%) probe elements on the GEM. Of those 324 (1.5% of the total possible elements and 79.4% of the significantly expressed elements) were up-regulated. The number of genes whose expression was down regulated was markedly less. 83 (0.4% of the total possible elements and 20.3% of the significantly expressed elements) genes were down-regulated at or above significant levels. In summary, the greatest number of significant changes in gene expression was in the up-regulated direction (nearly 4 times), and the greatest magnitude of change for single genes (over 2 times) was also up-regulation.

DISCUSSION

Selected genes and ESTs from Appendices A and B can be reviewed as to the physiological function and/or biological marker for which they are known whenever possible. Also note that the appendices contain ESTs that were differentially regulated by the cells post laser exposure. As of the date of the experimental analysis, the functions of the genes related to the above ESTs were not known. But recent updates of the NCBI genomic database, several ESTs in the appendices have been assigned

genetic/physiologic functions. However, other EST's that were differentially regulated functions remain unknown thus remain fertile ground for future exploration and analysis. Gene functions can easily be located through a PubMed query in the NCBI searchable database format found in the appendices.

These two experimental data sets are offered as a contribution to the continuing efforts in understanding the response of RPE to the exposure of high energy pulsed laser-light exposure using gene expression profiling 12 hours and 24 hours post-exposure. In the multi-dimensional hyper-volume of laser settings versus various tissues' response and time of response post-exposure, these can provide insights at specific matrix data points to possible perturbation to cellular physiology to include aspects of damage, repair and decreased/absent/rescued function.

Closing

As a closing comment we offer the following observation: These are the last gene expression profile experiments using Affymetrix GeneChip technology done in the Laser and Optics Research Center, Department of Physics, United States Air Force Academy. We highly recommend that this type of work, started here, be continued to aid in understanding the effect of laser-light exposure on affected human tissue. This use of living human cadaver donor tissue marks a major step forward toward assessing the cellular perturbation to be expected in the human organism and should be strongly considered as an experimental model until such time as the tissue microarray and organotypic model technologies more closely approximate the *in vivo* human response. We also suggest the employment of various statistical modeling techniques such as Taguchi's to establish the relevant orthogonal contrasts in the multi-dimensional hypervolume of laser settings versus biological response endpoints to rationally define the pertinent experimental data points to appropriately model laser-tissue interaction. In the context of more in depth analysis of the gene expression data, numerous higher order software platforms offer advance analyses, some employing artificial intelligence capabilities. As a closing thought we are attaching our concepts of future laser bioeffects research directions (Figure 5), a metabonomic risk assessment model of laser tissue interaction (Figure 6), and some suggestions for the transition to knowledge building/modeling from data collection (Figure 7) in laser bioeffects research.

Figure 1.

Fold Change: N2HX - Signal,CN2HX - Signal

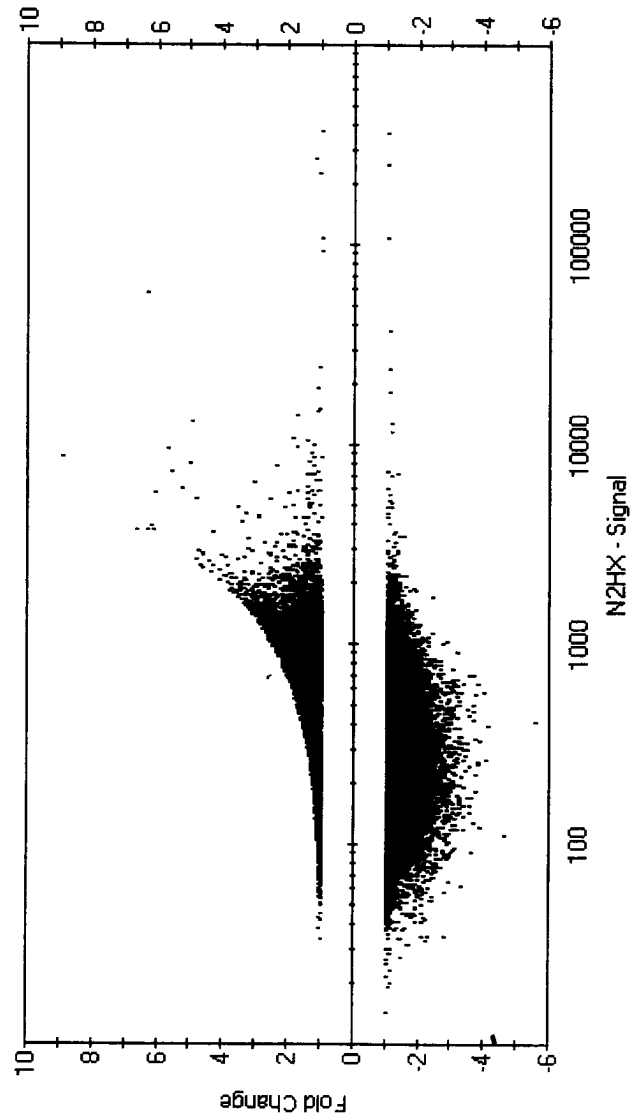


Figure 2.

Variable Bin Histogram

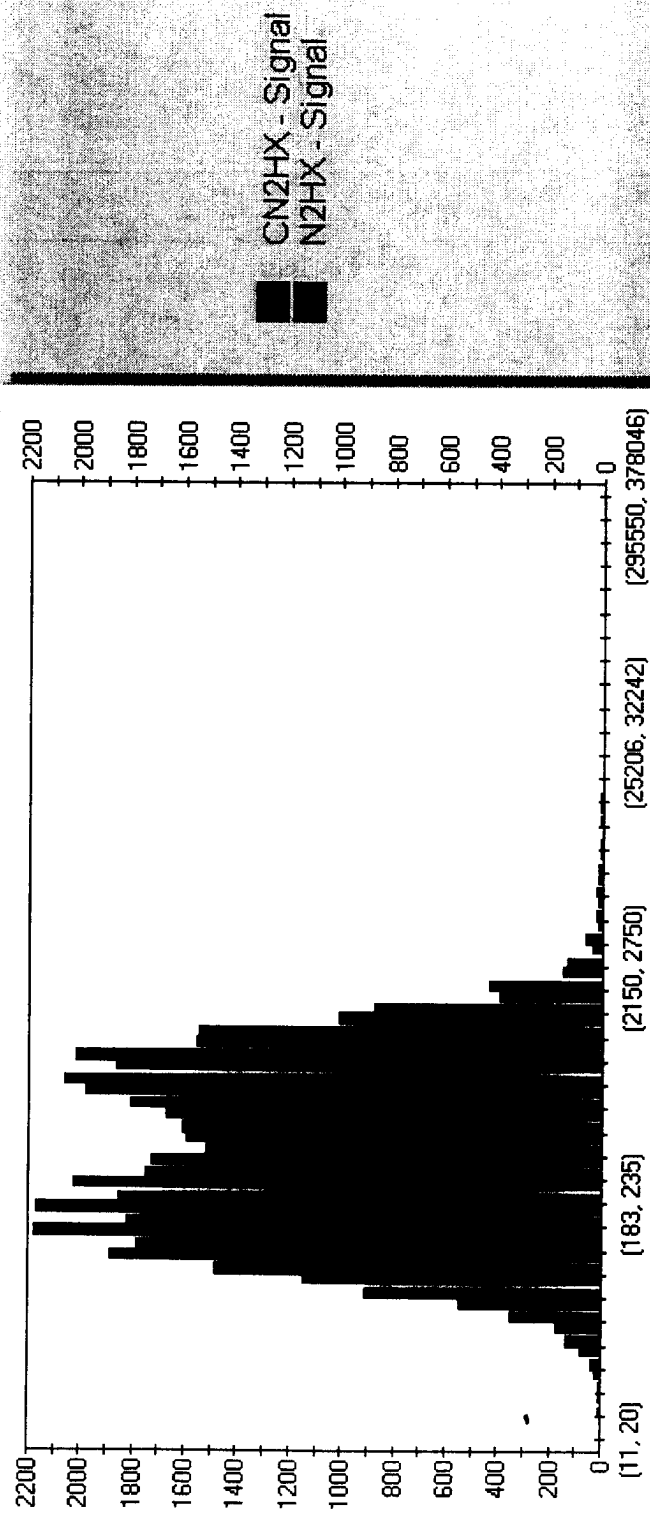


Figure 3.

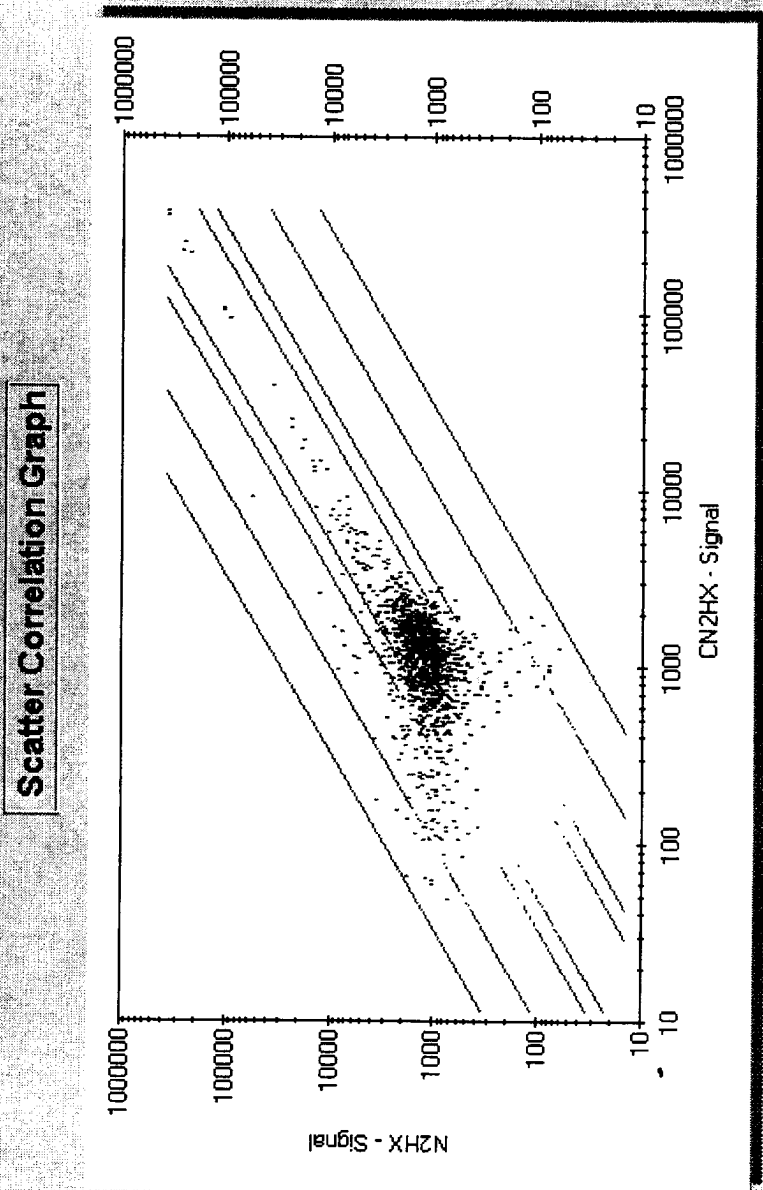


Figure 4.

Fold Change: P4HX12 - Signal,CP4HX12 - Signal

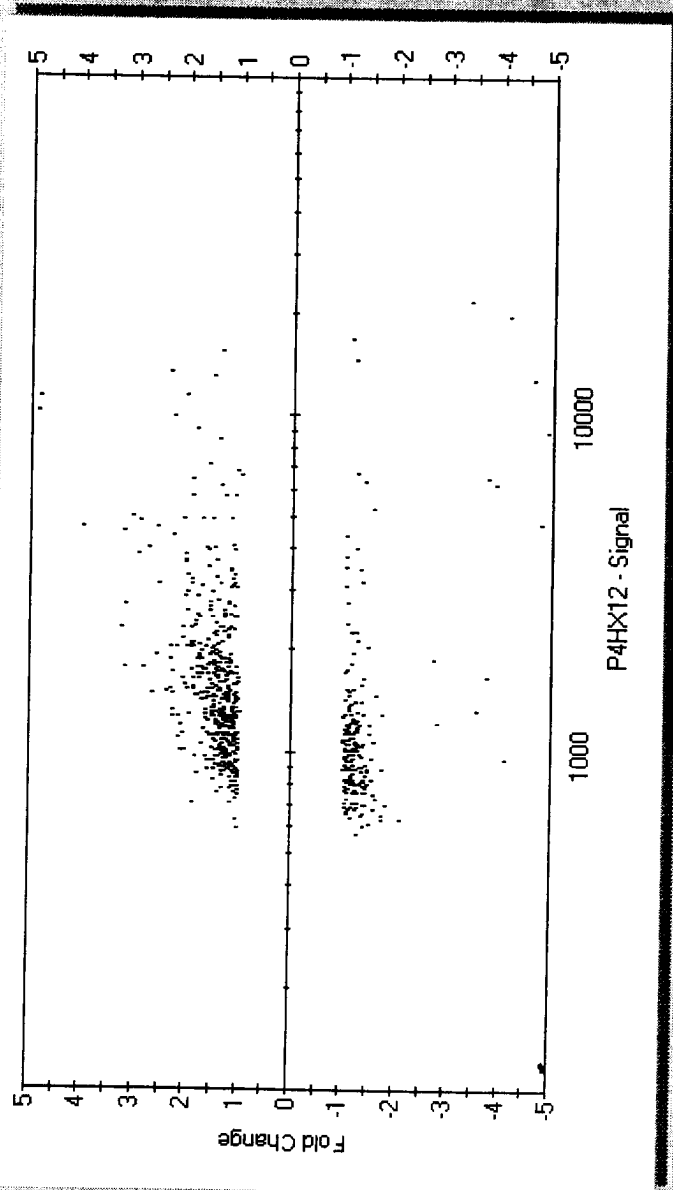


Figure 5.

LASER BIOEFFECTS

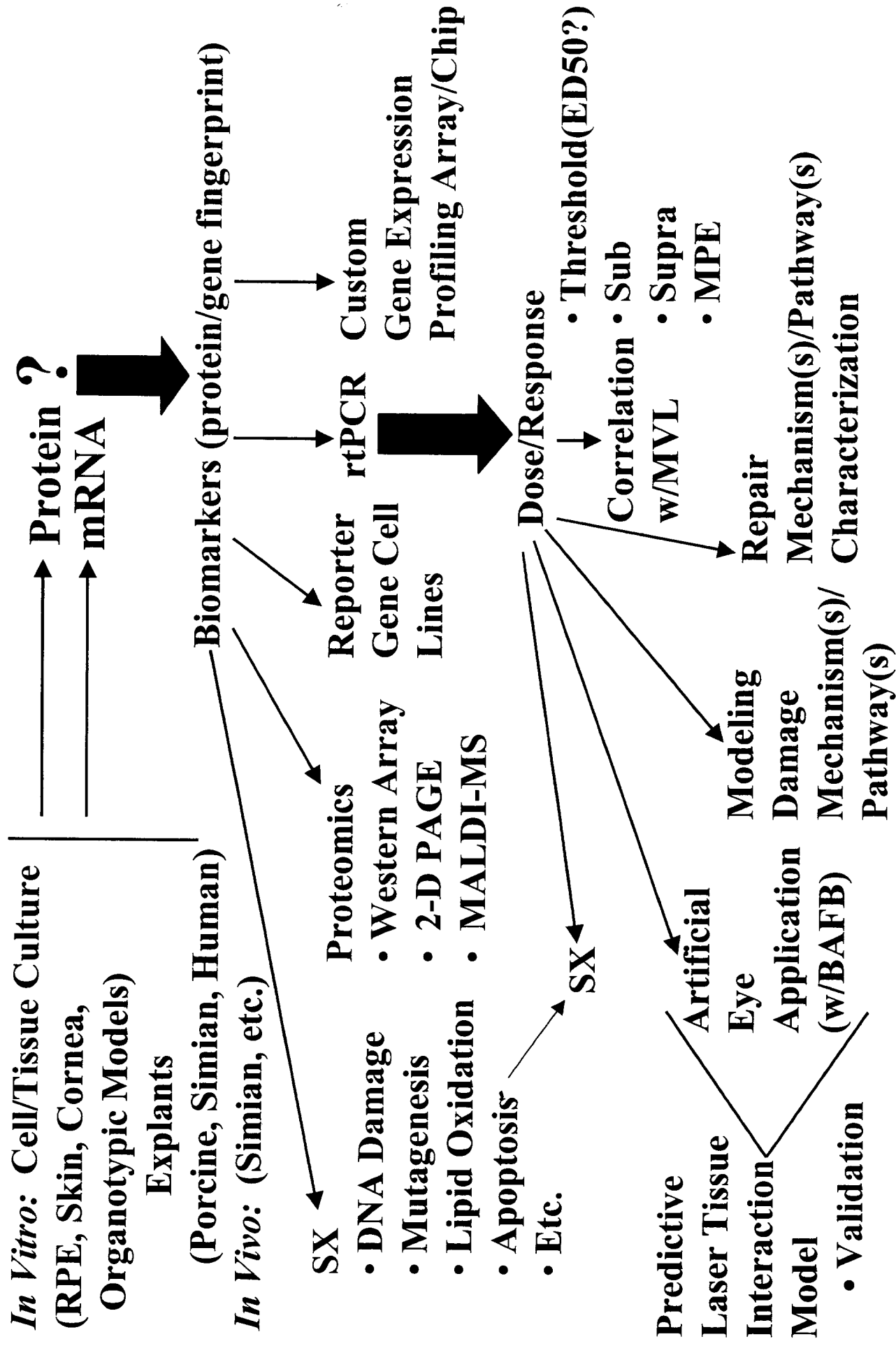


Figure 6.

METABONOMIC RISK ASSESSMENT

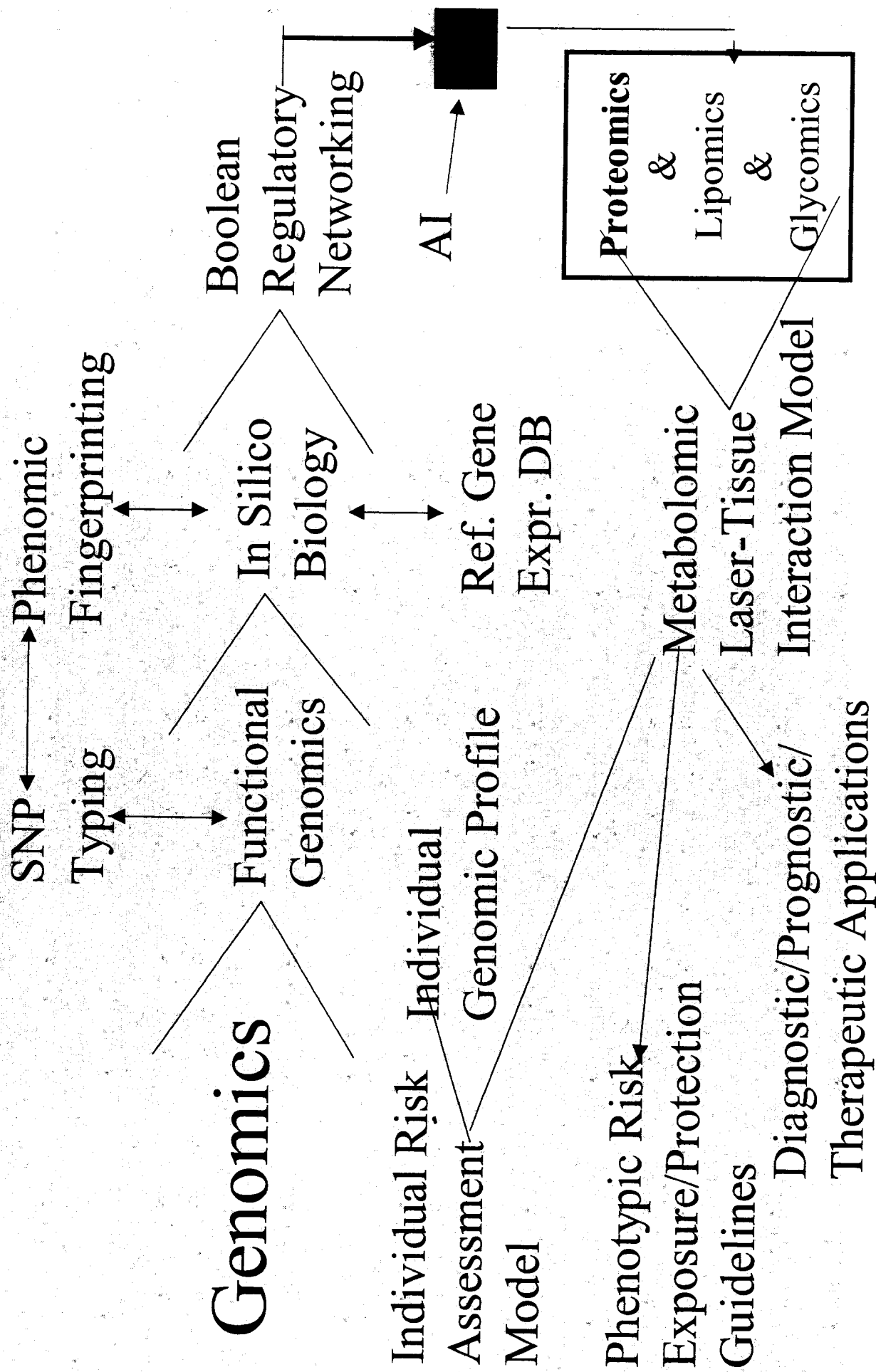


Figure 7.

- # KNOWLEDGE BUILDING
- (Transition from data collection)
- Statistical Design
 - Multi-Dimensional Hyper-Volume (laser settings)
 - Orthogonal Contrasts Drive Experimental Design
 - Biological Endpoints
 - Bioinformatics
 - Integrative Platform (data mining)
 - Central Repository
 - Biomarker Discovery/Validation
 - Retrospective Analysis-MVL
 - Clinical data correlated to histo/cell/molecular data
 - Exposures/Metabolic Homology/Bridging Experiments
 - Collaboration=Max. Efficiency/Integration/Holism

Appendix A.

| Probe set | CN2HX Signal | N2HX Signal | CN2 vs N2 Fold Change | Description |
|-------------|-----------------|----------------|--------------------------|--|
| 212917_x_at | 922.1 | 325.2 | -2.84 | Consensus includes gb:A1814728 /FEA=EST /DB_XREF=gi:5425943 /DB_XREF=est:wk66h11.x1 /CL |
| 217715_x_at | 2715.5 | 989 | -2.75 | Consensus includes gb:BE045142 /FEA=EST /DB_XREF=gi:8362195 /DB_XREF=est:hn26h02.x1 /C |
| 220625_s_at | 2057.1 | 822.4 | -2.5 | gb:AF115403.1 /DEF=Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds. /FEA=m |
| 214421_x_at | 2212.3 | 980.6 | -2.26 | Consensus includes gb:AV652420 /FEA=EST /DB_XREF=gi:9873434 /DB_XREF=est:AV652420 /CL |
| 215823_x_at | 1145.2 | 527.9 | -2.17 | Consensus includes gb:U64661 /DEF=Human poly(A)-blinding protein processed pseudogene3 /FE |
| 201060_x_at | 2178.8 | 1033.6 | -2.11 | Consensus includes gb:A1537887 /FEA=EST /DB_XREF=gi:4452022 /DB_XREF=est:tp32g06.x1 /CL |
| 218807_at | 2276.8 | 1078 | -2.11 | gb:NM_006113.2 /DEF=Homo sapiens vav 3 oncogene (VAV3), mRNA. /FEA=mRNA /GEN=VAV3 /Pt |
| 211504_x_at | 1971.2 | 1023.7 | -1.93 | gb:D87931.1 /DEF=Homo sapiens mRNA for Rho kinase, complete cds. /FEA=mRNA /PROD=Rho k |
| 207684_at | 1584.6 | 837.8 | -1.89 | gb:NM_004608.1 /DEF=Homo sapiens T-box 6 (TBX6), mRNA. /FEA=mRNA /GEN=TBX6 /PROD=T-b |
| 203758_at | 1343.5 | 714.1 | -1.88 | Consensus includes gb:AV729484 /FEA=EST /DB_XREF=gi:10838905 /DB_XREF=est:AV729484 /CL |
| 215112_x_at | 932.7 | 519.2 | -1.8 | Consensus includes gb:AB020668.1 /DEF=Homo sapiens mRNA for KIAA0861 protein, partial cds. |
| 208114_s_at | 2260.9 | 1268.9 | -1.78 | gb:NM_030980.1 /DEF=Homo sapiens hypothetical protein FLJ12671 (FLJ12671), mRNA. /FEA=mR |
| 213881_x_at | 2545.9 | 1440.9 | -1.77 | Consensus includes gb:A1971724 /FEA=EST /DB_XREF=gi:5768550 /DB_XREF=est:wr07a04.x1 /CL |
| 206434_at | 1636.1 | 962.6 | -1.7 | gb:NM_016950.1 /DEF=Homo sapiens testican 3 (HSAJ1454), mRNA. /FEA=mRNA /GEN=HSAJ1454 |
| 202594_at | 1182.6 | 699.7 | -1.69 | gb:NM_015344.1 /DEF=Homo sapiens MYO47 protein (MYO47), mRNA. /FEA=mRNA /GEN=MYO47 /P |
| 204252_at | 1613.4 | 970.3 | -1.66 | gb:M68520.1 /DEF=Human cdc2-related protein kinase mRNA, complete cds. /FEA=mRNA /PROD= |
| 217097_s_at | 1040.5 | 629.3 | -1.65 | Consensus includes gb:AC004990 /DEF=Homo sapiens PAC clone RP5-118517 from 7q11.23-q21 /F |
| 216801_at | 2056.3 | 1258 | -1.63 | Consensus includes gb:AK026910.1 /DEF=Homo sapiens cDNA: FLJ23257 fis, clone COL05579. /FI |
| 49327_at | 3438.9 | 2176.6 | -1.58 | Cluster Incl. A1492888:th78c09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2124784 /clone_end= |
| 212749_s_at | -1527.2 | 971.5 | -1.57 | Consensus includes gb:A1096477 /FEA=EST /DB_XREF=gi:3445971 /DB_XREF=est:qa03c06.x1 /CL |
| 222252_x_at | 3007.9 | 1920 | -1.57 | Consensus includes gb:AK023354.1 /DEF=Homo sapiens cDNA FLJ13292 fis, clone OVARC100118 |
| 207788_s_at | 1566.8 | 1025.8 | -1.53 | gb:NM_005775.1 /DEF=Homo sapiens vinexin beta (SH3-containing adaptor molecule-1) (SCAM-1), |
| 65635_at | 5209.2 | 3401.8 | -1.53 | Cluster Incl. AL044097:DKFP434M1928_s1 Homo sapiens cDNA, 3 end /clone=DKFP434M1928 /c |
| 207265_s_at | 2283 | 1502.5 | -1.52 | gb:NM_016657.1 /DEF=Homo sapiens KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein rete |
| 214222_at | 1673.7 | 1132.2 | -1.48 | Consensus includes gb:AB023161.1 /DEF=Homo sapiens mRNA for KIAA0944 protein, partial cds. |
| 214902_x_at | 2298 | 1556.6 | -1.48 | Consensus includes gb:AL080232.1 /DEF=Homo sapiens mRNA; cDNA DKFP586A061 (from clone |
| 49878_at | 3230.3 | 2181.2 | -1.48 | Cluster Incl. AA523441:ng30d08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-936303 /clone_end= |
| 212896_at | 879.8 | 612.4 | -1.44 | Consensus includes gb:D29641.2 /DEF=Homo sapiens mRNA for KIAA0052 protein, partial cds. /FE |
| 209130_at | 1213.7 | 845.8 | -1.43 | gb:BC003686.1 /DEF=Homo sapiens, synaptosomal-associated protein, 23kD, clone MGC:5155, mF |
| 218374_s_at | 1580.8 | 1110.2 | -1.42 | gb:NM_020374.1 /DEF=Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA. /F |
| 200630_x_at | 2728.4 | 1919.4 | -1.42 | Consensus includes gb:AV702810 /FEA=EST /DB_XREF=gi:10719140 /DB_XREF=est:AV702810 /CL |
| 220290_at | 1399.6 | 997.9 | -1.4 | gb:NM_017977.1 /DEF=Homo sapiens hypothetical protein FLJ10040 (FLJ10040), mRNA. /FEA=mR |

| | | | | |
|-------------|--------|--------|-------|--|
| 218020_s_at | 1899 | 1358.6 | -1.4 | gb:NM_021943.1 /DEF=Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA. /FEA=mRNA |
| 211918_x_at | 2309.7 | 1654.7 | -1.4 | gb:AF311940.1 /DEF=Homo sapiens pregnancy-associated plasma preproprotein-A2 mRNA, comp |
| 200662_s_at | 2076.6 | 1499 | -1.39 | gb:NM_014765.1 /DEF=Homo sapiens translocase of outer mitochondrial membrane 20 (yeast) hor |
| 208020_s_at | 1272 | 923.7 | -1.38 | gb:NM_000719.1 /DEF=Homo sapiens calcium channel, voltage-dependent, L type, alpha 1C subur |
| 212261_at | 2753.3 | 2006.7 | -1.37 | Consensus includes gb:AB014542.1 /DEF=Homo sapiens mRNA for KIAA0642 protein, partial cds. |
| 200012_x_at | 1571.5 | 1155.6 | -1.36 | gb:NM_000982.1 /DEF=Homo sapiens ribosomal protein L21 (gene or pseudogene) (RPL21), mRN/ |
| 222370_x_at | 1986.5 | 1458.4 | -1.36 | Consensus includes gb:N57781 /FEA=EST /DB_XREF=gi:1201671 /DB_XREF=est:yv56g05.s1 /CLO |
| 56197_at | 3832.8 | 2838.1 | -1.35 | Cluster Incl. AI783924:tr30e11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2219852 /clone_end= |
| 217497_at | 1261.3 | 943.1 | -1.34 | Consensus includes gb:AW613387 /FEA=EST /DB_XREF=gi:7318573 /DB_XREF=est:hh71e04.x1 /C |
| 213226_at | 1237.6 | 930.3 | -1.33 | Consensus includes gb:AI346350 /FEA=EST /DB_XREF=gi:4083556 /DB_XREF=est:qp50c06.x1 /C |
| 213798_s_at | 2376.8 | 1780.5 | -1.33 | Consensus includes gb:AA806142 /FEA=EST /DB_XREF=gi:2874892 /DB_XREF=est:oe29d06.s1 /C |
| 200763_s_at | 2612.7 | 1974.5 | -1.32 | gb:NM_001003.1 /DEF=Homo sapiens ribosomal protein, large, P1 (RPLP1), mRNA. /FEA=mRNA /C |
| 220015_at | 2899.9 | 2204.7 | -1.32 | gb:NM_017766.1 /DEF=Homo sapiens hypothetical protein FLJ20321 (FLJ20321), mRNA. /FEA=mR |
| 216187_x_at | 9297 | 7096.3 | -1.31 | Consensus includes gb:AF222691.1 /DEF=Homo sapiens Alu repeat (LNX1) mRNA sequence. /FEA |
| 215019_x_at | 3189.9 | 2462.1 | -1.3 | Consensus includes gb:AW474158 /FEA=EST /DB_XREF=gi:7044264 /DB_XREF=est:xy11f01.x1 /C |
| 222329_x_at | 4701.1 | 3629.1 | -1.3 | Consensus includes gb:AW974816 /FEA=EST /DB_XREF=gi:8166019 /DB_XREF=est:EST386921 /U |
| 219938_s_at | 1194.6 | 922.6 | -1.29 | gb:NM_024430.1 /DEF=Homo sapiens proline-serine-threonine phosphatase interacting protein 2 (|
| 218143_s_at | 2299.2 | 1781.5 | -1.29 | gb:NM_005697.2 /DEF=Homo sapiens secretory carrier membrane protein 2 (SCAMP2), mRNA. /FE |
| 206916_x_at | 2861.6 | 2235.8 | -1.28 | gb:NM_000353.1 /DEF=Homo sapiens tyrosine aminotransferase (TAT), nuclear gene encoding mit |
| 214034_at | 1326.9 | 1046.8 | -1.27 | Consensus includes gb:AB011097.1 /DEF=Homo sapiens mRNA for KIAA0525 protein, partial cds. |
| 201143_s_at | 1136.1 | 901.9 | -1.26 | gb:BC002513.1 /DEF=Homo sapiens, eukaryotic translation initiation factor 2, subunit 1 (alpha, 35) |
| 210927_x_at | 1777.1 | 1412.7 | -1.26 | gb:BC004239.1 /DEF=Homo sapiens, jumping translocation breakpoint, clone MGC:10274, mRNA, |
| 215478_at | 1388.9 | 1111.4 | -1.25 | Consensus includes gb:AF007156.1 /DEF=Homo sapiens clone 23617 unknown mRNA, partial cds. |
| 217406_at | 1932.6 | 1548.7 | -1.25 | Consensus includes gb:AL021937 /DEF=Human DNA sequence from clone RP1-149A16 on chromo |
| 215607_x_at | 2606 | 2076.8 | -1.25 | Consensus includes gb:AU144530 /FEA=EST /DB_XREF=gi:11006051 /DB_XREF=est:AU144530 /C |
| 214869_x_at | 1127.2 | 910 | -1.24 | Consensus includes gb:AK021533.1 /DEF=Homo sapiens cDNA FLJ11471 fis, clone HEMBA100167 |
| 210840_s_at | 1563.4 | 1269.9 | -1.23 | gb:D29640.1 /DEF=Human mRNA for KIAA0051 gene, complete cds. /FEA=mRNA /GEN=KIAA0051 |
| 214135_at | 1740.1 | 1417.9 | -1.23 | Consensus includes gb:BE551219 /FEA=EST /DB_XREF=gi:9792911 /DB_XREF=est:7b56b11.x1 /C |
| 203899_s_at | 1780.4 | 1448.8 | -1.23 | gb:NM_014478.1 /DEF=Homo sapiens calcitonin gene-related peptide-receptor component protein |
| 213612_x_at | 2957.5 | 2397.5 | -1.23 | Consensus includes gb:AI800419 /FEA=EST /DB_XREF=gi:5365891 /DB_XREF=est:ij14b09.x1 /CLC |
| 35150_at | 3243.7 | 2635.7 | -1.23 | Cluster Incl. X60592:Human CD40 mRNA for nerve growth factor receptor-related B-lymphocyte z |
| 206336_at | 1133.4 | 932.4 | -1.22 | gb:NM_002993.1 /DEF=Homo sapiens small inducible cytokine subfamily B (Cys-X-Cys), member 6 |
| 216993_s_at | 3147.8 | 2583.4 | -1.22 | Consensus includes gb:U32169 /DEF=Human pro-a2 chain of collagen type XI (COL11A2) gene, co |
| 211115_x_at | 1285 | 1064.1 | -1.21 | gb:AB037703.1 /DEF=Homo sapiens SIP1-delta mRNA for SMN interacting protein 1-delta, complet |
| 217484_at | 1593.5 | 1326.5 | -1.2 | Consensus includes gb:X14362.1 /DEF=Human CR1 mRNA for C3bC4b receptor secreted form. /FE |

| | | | | |
|-------------|--------|--------|------|--|
| 203297_s_at | 2019.8 | 1685.1 | -1.2 | Consensus includes gb:BG029530 /FEA=EST /DB_XREF=gi:12418626 /DB_XREF=est:602297090F1 |
| 36888_at | 4267.1 | 3560.4 | -1.2 | Cluster Incl. AB020648:Homo sapiens mRNA for KIAA0841 protein, partial cds /cds=(0,1925) /gb=p |
| 216220_s_at | 1209.3 | 1462.8 | 1.21 | Consensus includes gb:X68485.1 /DEF=H.sapiens mRNA for A1 adenosine receptor. /FEA=mRNA |
| 201649_at | 1602.4 | 1937.1 | 1.21 | gb:NM_004223.1 /DEF=Homo sapiens ubiquitin-conjugating enzyme E2L 6 (UBE2L6), mRNA. /FEA |
| 218269_at | 1044.9 | 1269.9 | 1.22 | gb:NM_013235.1 /DEF=Homo sapiens putative ribonuclease III (RNASE3L), mRNA. /FEA=mRNA /G |
| 204517_at | 1136.1 | 1388.4 | 1.22 | Consensus includes gb:BE962749 /FEA=EST /DB_XREF=gi:11765968 /DB_XREF=est:601656143R1 |
| 219410_at | 1165.6 | 1426.8 | 1.22 | gb:NM_018004.1 /DEF=Homo sapiens hypothetical protein FLJ10134 (FLJ10134), mRNA. /FEA=mR |
| 221158_at | 1402.6 | 1708.3 | 1.22 | gb:NM_013329.1 /DEF=Homo sapiens GC-rich sequence DNA-binding factor candidate (GCFC), m |
| 215383_x_at | 3715.8 | 4515.3 | 1.22 | Consensus includes gb:AL137312.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761K23121 (from cl |
| 217810_x_at | 2031.2 | 2504.9 | 1.23 | gb:NM_020117.1 /DEF=Homo sapiens hypothetical protein FLJ10595 (FLJ10595), mRNA. /FEA=mR |
| 216159_s_at | 1206.8 | 1512.8 | 1.25 | Consensus includes gb:AK023757.1 /DEF=Homo sapiens cDNA FLJ13695 fis, clone PLACE200012 |
| 208591_s_at | 1688.9 | 2110.3 | 1.25 | gb:NM_000922.1 /DEF=Homo sapiens phosphodiesterase 3B, cGMP-inhibited (PDE3B), mRNA. /FE |
| 200989_at | 1704 | 2154.2 | 1.26 | gb:NM_001530.1 /DEF=Homo sapiens hypoxia-inducible factor 1, alpha subunit (basic helix-loop-h |
| 201404_x_at | 4464.7 | 5656.3 | 1.27 | gb:BC000268.1 /DEF=Homo sapiens, proteasome (prosome, macropain) subunit, beta type, 2, clon |
| 206792_x_at | 7879.1 | 9990 | 1.27 | gb:NM_000923.1 /DEF=Homo sapiens phosphodiesterase 4C, cAMP-specific (dunce (Drosophila)- |
| 212208_at | 1460.7 | 1877.9 | 1.29 | Consensus includes gb:AK023837.1 /DEF=Homo sapiens cDNA FLJ13775 fis, clone PLACE400036 |
| 220352_x_at | 1469.7 | 1925.3 | 1.31 | gb:NM_024305.1 /DEF=Homo sapiens hypothetical protein MGC4278 (MGC4278), mRNA. /FEA=mR |
| 212607_at | 2235.8 | 2928.8 | 1.31 | Consensus includes gb:AK024958.1 /DEF=Homo sapiens cDNA: FLJ21305 fis, clone COL02124. /F |
| 215588_x_at | 3831.3 | 5021.2 | 1.31 | Consensus includes gb:AK024958.1 /DEF=Homo sapiens cDNA: FLJ21305 fis, clone COL02124. /F |
| 220796_x_at | 6875.1 | 8986.1 | 1.31 | gb:NM_024881.1 /DEF=Homo sapiens hypothetical protein FLJ14251 (FLJ14251), mRNA. /FEA=mR |
| 207783_x_at | 1864.1 | 2466.5 | 1.32 | gb:NM_017627.1 /DEF=Homo sapiens hypothetical protein FLJ20030 (FLJ20030), mRNA. /FEA=mR |
| 213030_s_at | 666.3 | 899.9 | 1.35 | Consensus includes gb:AI688418 /FEA=EST /DB_XREF=gi:4899712 /DB_XREF=est:wc94h03.x1 /C1 |
| 40420_at | 991.1 | 1337.6 | 1.35 | Cluster Incl. AB015718:Homo sapiens lok mRNA for protein kinase, complete cds /cds=(50,2956) / |
| 213507_s_at | 1552 | 2096.6 | 1.35 | Consensus includes gb:BG249565 /FEA=EST /DB_XREF=gi:12759381 /DB_XREF=est:602319636F1 |
| 214672_at | 1262.1 | 1714.5 | 1.36 | Consensus includes gb:AB023215.1 /DEF=Homo sapiens mRNA for KIAA0998 protein, partial cds. |
| 209927_s_at | 1374.9 | 1872.5 | 1.36 | gb:AF261137.1 /DEF=Homo sapiens HT031 mRNA, complete cds. /FEA=mRNA /PROD=HT031 /DB_ |
| 215604_x_at | 1875.3 | 2557.5 | 1.36 | Consensus includes gb:AK023783.1 /DEF=Homo sapiens cDNA FLJ13721 fis, clone PLACE200045 |
| 214022_s_at | 5238.3 | 7138 | 1.36 | Consensus includes gb:AA749101 /FEA=EST /DB_XREF=gi:2789059 /DB_XREF=est:ny11d02.s1 /C |
| 121_at | 3601.5 | 4958.8 | 1.38 | X69699 /FEATURE= /DEFINITION=HSPAX8A H.sapiens Pax8 mRNA |
| 215303_at | 666.4 | 925 | 1.39 | Consensus includes gb:BE046461 /FEA=EST /DB_XREF=gi:8363514 /DB_XREF=est:hn47g05.x2 /C |
| 215179_x_at | 3502.6 | 4858.3 | 1.39 | Consensus includes gb:AK023843.1 /DEF=Homo sapiens cDNA FLJ13781 fis, clone PLACE400046: |
| 208120_x_at | 5959.6 | 8319.7 | 1.4 | gb:NM_031221.1 /DEF=Homo sapiens hypothetical protein FKSG63 (FKSG63), mRNA. /FEA=mRNA |
| 211040_x_at | 2034.3 | 2862.8 | 1.41 | gb:BC006325.1 /DEF=Homo sapiens, G-2 and S-phase expressed 1, clone MGC:12560, mRNA, com |
| 214473_x_at | 1096.5 | 1561.5 | 1.42 | Consensus includes gb:NM_005395.1 /DEF=Homo sapiens postmeiotic segregation increased 2-lik |
| 55705_at | 3787.7 | 5368.6 | 1.42 | Cluster Incl. W07773:zb03g04.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-301014 /clone_end=5 |

| | | | | |
|-------------|---------|---------|------|--|
| 214715_x_at | 5050.3 | 7190 | 1.42 | Consensus includes gb:AK024789.1 /DEF=Homo sapiens cDNA: FLJ21136 fls, clone CAS07469. /FE |
| 210686_x_at | 3960.6 | 5675.8 | 1.43 | gb:BC001407.1 /DEF=Homo sapiens, Similar to cytochrome c-like antigen, clone MGC:2960, mRNA |
| 209057_x_at | 7271.8 | 10405.8 | 1.43 | gb:AB007892.1 /DEF=Homo sapiens KIAA0432 mRNA, complete cds. /FEA=mRNA /GEN=KIAA0432 |
| 215726_s_at | 1179.8 | 1693.4 | 1.44 | Consensus includes gb:M22976.1 /DEF=Human cytochrome b5 mRNA, 3 end. /FEA=mRNA /GEN=C |
| 219206_x_at | 1491.5 | 2145.1 | 1.44 | gb:NM_016056.1 /DEF=Homo sapiens CGI-119 protein (LOC51643), mRNA. /FEA=mRNA /GEN=LOC |
| 215628_x_at | 4210.6 | 6154.8 | 1.46 | Consensus includes gb:AL049285.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564M193 (from clone |
| 206936_x_at | 2925.9 | 4313.7 | 1.47 | gb:NM_022335.1 /DEF=Homo sapiens hypothetical protein PRO2849 (PRO2849), mRNA. /FEA=mRN |
| 211600_at | 2704.1 | 4012.4 | 1.48 | gb:U20489.1 /DEF=Human glomerular epithelial protein 1 (GLEPP1) mRNA, complete cds. /FEA=mR |
| 204246_s_at | 1387.3 | 2091.5 | 1.51 | gb:NM_007234.2 /DEF=Homo sapiens dynactin 3 (p22) (DCTN3), transcript variant 1, mRNA. /FEA=mR |
| 203406_at | 1483.7 | 2252.8 | 1.52 | gb:NM_005926.1 /DEF=Homo sapiens microfilament-associated protein 1 (MFAP1), mRNA. /FEA=mR |
| 212639_x_at | 2227.4 | 3412.4 | 1.53 | Consensus includes gb:AL581768 /FEA=EST /DB_XREF=gi:12949093 /DB_XREF=est:AL581768 /CL |
| 216054_x_at | 1106.7 | 1706.5 | 1.54 | Consensus includes gb:X58851 /DEF=Human MLC1emb gene for embryonic myosin alkaline light c |
| 212735_at | 1180.3 | 1817.6 | 1.54 | Consensus includes gb:BF448041 /FEA=EST /DB_XREF=gi:11513102 /DB_XREF=est:7q97f09.x1 /C |
| 201922_at | 1634.7 | 2536 | 1.55 | gb:NM_014886.1 /DEF=Homo sapiens hypothetical protein (YR-29), mRNA. /FEA=mRNA /GEN=YR-2 |
| 212284_x_at | 1858.2 | 2899.4 | 1.56 | Consensus includes gb:BG498776 /FEA=EST /DB_XREF=gi:13460293 /DB_XREF=est:602544416F1 |
| 206940_s_at | 1046.6 | 1648.6 | 1.58 | gb:NM_006237.1 /DEF=Homo sapiens POU domain, class 4, transcription factor 1 (POU4F1), mRNA |
| 218171_at | 909 | 1449.5 | 1.59 | gb:AF195514.1 /DEF=Homo sapiens VPS4-2 ATPase (VPS42) mRNA, complete cds. /FEA=mRNA /G |
| 203480_s_at | 1245.5 | 1976.3 | 1.59 | gb:NM_014928.1 /DEF=Homo sapiens KIAA1046 protein (KIAA1046), mRNA. /FEA=mRNA /GEN=KIA |
| 207990_x_at | 1146.1 | 1838.9 | 1.6 | gb:NM_020114.1 /DEF=Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript variant 9, mR |
| 221435_x_at | 881.7 | 1427.6 | 1.62 | gb:NM_031207.1 /DEF=Homo sapiens hypothetical protein HT036 (HT036), mRNA. /FEA=CDS /GEN |
| 203504_s_at | 603.2 | 1002.4 | 1.66 | gb:NM_005502.1 /DEF=Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABC |
| 208780_x_at | 1121.1 | 1930.1 | 1.72 | gb:AF154847.1 /DEF=Homo sapiens 33 kDa Vamp-associated protein (VAMP) mRNA, complete cds |
| 210739_x_at | -2020.1 | 3496 | 1.73 | gb:AF069510.1 /DEF=Homo sapiens sodium bicarbonate cotransporter (NBC) mRNA, complete cds |
| 205370_x_at | 8100.3 | 14071.5 | 1.74 | gb:NM_001918.1 /DEF=Homo sapiens dihydrolipoamide branched chain transacylase (E2 compone |
| 201575_at | 1246.3 | 2182.3 | 1.75 | gb:NM_012245.1 /DEF=Homo sapiens SKI-INTERACTING PROTEIN (SNW1), mRNA. /FEA=mRNA /G |
| 208246_x_at | 3369.8 | 5918.3 | 1.76 | gb:NM_017618.1 /DEF=Homo sapiens hypothetical protein FLJ20006 (FLJ20006), mRNA. /FEA=mR |
| 211452_x_at | 2358.7 | 4248.9 | 1.8 | gb:AF130054.1 /DEF=Homo sapiens clone FLB4816 PRO1252 mRNA, complete cds. /FEA=mRNA /P |
| 217918_at | 1771.8 | 3279.7 | 1.85 | gb:NM_014183.1 /DEF=Homo sapiens HSPC162 protein (HSPC162), mRNA. /FEA=mRNA /GEN=HSP |
| 220071_x_at | 2615.6 | 4959.7 | 1.9 | gb:NM_018097.1 /DEF=Homo sapiens hypothetical protein FLJ10460 (FLJ10460), mRNA. /FEA=mR |
| 220232_at | 5702.1 | 10811.6 | 1.9 | gb:NM_024906.1 /DEF=Homo sapiens hypothetical protein FLJ21032 (FLJ21032), mRNA. /FEA=mR |
| 213382_at | 783.7 | 1516.9 | 1.94 | Consensus includes gb:AL137798 /DEF=Human DNA sequence from clone RP5-1182A14 on chrom |
| 213835_x_at | 2887.1 | 5764.6 | 2 | Consensus includes gb:AL524262 /FEA=EST /DB_XREF=gi:12787755 /DB_XREF=est:AL524262 /CL |
| 210319_x_at | 746.5 | 1500 | 2.01 | gb:D89377.1 /DEF=Homo sapiens mRNA for MSX-2, complete cds. /FEA=mRNA /PROD=MSX-2 /DB |
| 208869_s_at | 690.2 | 1436.2 | 2.08 | gb:AF087847.1 /DEF=Homo sapiens GABA-A receptor-associated protein like 1 (GABARAPL1) mR |
| 213936_x_at | 997.9 | 2086 | 2.09 | Consensus includes gb:AW276646 /FEA=EST /DB_XREF=gi:6663676 /DB_XREF=est:xr17f12.x1 /CL |

| | | | | |
|-------------|--------|---------|------|---|
| 44783_s_at | 2252.2 | 4775.3 | 2.12 | Cluster Incl. R61374:yh15e02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-37665 /clone_end=3 / |
| 216989_at | 685 | 1601.8 | 2.34 | Consensus includes gb:L13779.1 /DEF=Homo sapiens (clone H16) sperm surface protein PH-20 m |
| 208855_s_at | 904.2 | 2179.2 | 2.41 | gb:AF083420.1 /DEF=Homo sapiens brain-specific STE20-like protein kinase 3 (STK3) mRNA, com |
| 200759_x_at | 2062.8 | 5302 | 2.57 | gb:NM_003204.1 /DEF=Homo sapiens nuclear factor (erythroid-derived 2)-like 1 (NFE2L1), mRNA. |
| 200095_x_at | 2102.2 | 6436.5 | 3.06 | Consensus includes gb:AA320764 /FEA=EST /DB_XREF=gi:1973113 /DB_XREF=est:EST23183 /UG |
| 35201_at | 1196.1 | 4106.8 | 3.43 | Cluster Incl. X16135:Human mRNA for novel heterogeneous nuclear RNP protein, L protein /cds=(|
| 201429_s_at | 2608.6 | 12987.4 | 4.98 | gb:NM_000998.1 /DEF=Homo sapiens ribosomal protein L37a (RPL37A), mRNA. /FEA=mRNA /GEN |
| 208845_at | 1136.5 | 6016.2 | 5.29 | gb:BC002456.1 /DEF=Homo sapiens, voltage-dependent anion channel 3, clone MGC:1966, mRNA, |
| 201358_s_at | 1664.1 | 9562.7 | 5.75 | gb:NM_016451.1 /DEF=Homo sapiens coatomer protein complex, subunit beta (COPB), mRNA. /FE |
| 214041_x_at | 9133.1 | 57937.9 | 6.34 | Consensus includes gb:BE857772 /FEA=EST /DB_XREF=gi:10372131 /DB_XREF=est:7d62a11.x1 /C |

| Probe set | CP4HX12 P4HX12 | | CP4 vs P4 Fold Change | Description |
|-------------|----------------|--------|--------------------------|--|
| | Signal | Signal | | |
| 205430_at | 1308.1 | 628.6 | -2.08 | Consensus includes gb:AL133386 /DEF=Human DNA sequence from clone RP1-181C24 on chromosome 6 |
| 201742_x_at | 1249 | 697 | -1.79 | gb:Nm_006924.1 /DEF=Homo sapiens splicing factor, arginineserine-rich 1 (splicing factor 2, alternate splicing factor 2) |
| 206247_at | 1119.8 | 644.7 | -1.74 | gb:Nm_005931.1 /DEF=Homo sapiens MHC class I polypeptide-related sequence B (MICB), mRNA. /FEA=Homo sapiens |
| 213031_s_at | 1537.9 | 886.6 | -1.73 | Consensus includes gb:AF161382.1 /DEF=Homo sapiens HSPC264 mRNA, partial cds. /FEA=mRNA /PROC |
| 214321_at | 1076.1 | 624.6 | -1.72 | Consensus includes gb:BF440025 /FEA=EST /DB_XREF=gi:11452542 /DB_XREF=est:nac52c12.x1 /CLONE |
| 201540_at | 2224.9 | 1296.5 | -1.72 | gb:Nm_001449.1 /DEF=Homo sapiens four and a half LIM domains 1 (FHL1), mRNA. /FEA=mRNA /GEN=Homo sapiens |
| 205549_at | 2372.6 | 1470.7 | -1.61 | gb:Nm_006198.1 /DEF=Homo sapiens Purkinje cell protein 4 (PCP4), mRNA. /FEA=mRNA /GEN=PCP4 /PR |
| 201427_s_at | 1154 | 723.3 | -1.6 | gb:Nm_005410.1 /DEF=Homo sapiens selenoprotein P, plasma, 1 (SEPP1), mRNA. /FEA=mRNA /GEN=SEPP1 |
| 206297_at | 1678.6 | 1062.2 | -1.58 | gb:Nm_007272.1 /DEF=Homo sapiens chymotrypsin C (caldecrin) (CTRC), mRNA. /FEA=mRNA /GEN=CTRC |
| 205506_at | 1056.1 | 676.8 | -1.56 | gb:Nm_007127.1 /DEF=Homo sapiens villin 1 (VIL1), mRNA. /FEA=mRNA /GEN=villin 1 /DB_XREF= |
| 205006_s_at | 1159 | 741.8 | -1.56 | gb:Nm_004808.1 /DEF=Homo sapiens N-myristoyltransferase 2 (NMT2), mRNA. /FEA=mRNA /GEN=NMT2 / |
| 200018_at | 8197 | 5297.4 | -1.55 | gb:Nm_001017.1 /DEF=Homo sapiens ribosomal protein S13 (RPS13), mRNA. /FEA=mRNA /GEN=RPS13 /P |
| 213513_x_at | 1480.6 | 959.2 | -1.54 | Consensus includes gb:BG034239 /FEA=EST /DB_XREF=gi:12427339 /DB_XREF=est:602302301F1 /CLON |
| 210448_s_at | 1254.8 | 826.5 | -1.52 | gb:U49396.1 /DEF=Human ATP receptor P2X5b mRNA, complete cds. /FEA=mRNA /PROD=P2X |
| 201592_at | 1686.1 | 1131.9 | -1.49 | gb:Nm_003756.1 /DEF=Homo sapiens eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD) (E |
| 213878_at | 907 | 613.9 | -1.48 | Consensus includes gb:A1685944 /FEA=EST /DB_XREF=gi:4897238 /DB_XREF=est:tu38g02.x1 /CLONE=IM |
| 200799_at | 1778.3 | 1200.2 | -1.48 | gb:Nm_005345.3 /DEF=Homo sapiens heat shock 70kD protein 1A (HSPA1A), mRNA. /FEA=mRNA /GEN=H |
| 202787_s_at | 1181.7 | 805.5 | -1.47 | gb:U43784.1 /DEF=Human mitogen activated protein kinase activated protein kinase-3 mRNA, complete cd |
| 203278_s_at | 1275.2 | 871.8 | -1.46 | gb:Nm_016621.1 /DEF=Homo sapiens hypothetical protein (LOC51317), mRNA. /FEA=mRNA /GEN=LOC51 |
| 203885_at | 1299.4 | 889.3 | -1.46 | gb:Nm_014999.1 /DEF=Homo sapiens KIAA0118 protein (KIAA0118), mRNA. /FEA=mRNA /GEN=KIAA0118 |
| 208405_s_at | 2947.3 | 2049.2 | -1.44 | gb:Nm_006016.1 /DEF=Homo sapiens CD164 antigen, sialomucin (CD164), mRNA. /FEA=mRNA /GEN=CD1 |
| 215203_at | 993.6 | 693.1 | -1.43 | Consensus includes gb:AW438464 /FEA=EST /DB_XREF=gi:6973770 /DB_XREF=est:xu43g07.x1 /CLONE= |
| 201200_at | 1078.7 | 759.5 | -1.42 | gb:Nm_003851.1 /DEF=Homo sapiens cellular repressor of E1A-stimulated genes (CREG), mRNA. /FEA=m |
| 202388_at | 1118.4 | 786.8 | -1.42 | gb:Nm_002923.1 /DEF=Homo sapiens regulator of G-protein signalling 2, 24kD (RGS2), mRNA. /FEA=mRN |
| 213319_s_at | 1191 | 844.3 | -1.41 | Consensus includes gb:AW170359 /FEA=EST /DB_XREF=gi:6401884 /DB_XREF=est:xn60c12.x1 /CLONE= |
| 208116_s_at | 1066.9 | 759.8 | -1.4 | gb:Nm_005907.1 /DEF=Homo sapiens mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA. /FEA=m |
| 221435_x_at | 1087.8 | 776.4 | -1.4 | gb:Nm_031207.1 /DEF=Homo sapiens hypothetical protein HT036 (HT036), mRNA. /FEA=CDS /GEN=HT036 |
| 203563_at | 1279.2 | 915 | -1.4 | gb:Nm_021638.1 /DEF=Homo sapiens actin filament associated protein (AFAP), mRNA. /FEA=mRNA /GEN |
| 204234_s_at | 835 | 602.8 | -1.39 | Consensus includes gb:A1476267 /FEA=EST /DB_XREF=gi:4329312 /DB_XREF=est:ti72g01.x1 /CLONE=IM |
| 220059_at | 910.6 | 656.2 | -1.39 | gb:Nm_012108.1 /DEF=Homo sapiens BCR downstream signaling 1 (BRDG1), mRNA. /FEA=mRNA /GEN=B |
| 207719_x_at | 959.6 | 692.8 | -1.39 | gb:Nm_014812.1 /DEF=Homo sapiens KIAA0470 gene product (KIAA0470), mRNA. /FEA=mRNA /GEN=KIA |
| 204372_s_at | 1119.3 | 810.5 | -1.38 | gb:Nm_003685.1 /DEF=Homo sapiens KH-type splicing regulatory protein (FUSE binding protein 2) (KHSP |

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|-------------|--------|--------|-------|--|
| 212181_s_at | 2279.7 | 1650.7 | -1.38 | Consensus includes gb:AF191654.2 /DEF=Homo sapiens diposphoinositol polyphosphate phosphohydr |
| 211395_x_at | 1040 | 759.1 | -1.37 | gb:U0940.1 /DEF=Homo sapiens cell-type natural killer cells Fc gamma receptor Ilc3 (Fc-gammaRIIC) mR |
| 218323_at | 1087.6 | 795.2 | -1.37 | gb:N18307.1 /DEF=Homo sapiens hypothetical protein FLJ11040 (FLJ11040), mRNA. /FEA=mRNA /GE |
| 206833_s_at | 1124.2 | 820.9 | -1.37 | gb:N1001108.1 /DEF=Homo sapiens acylphosphatase 2, muscle type (ACYP2), mRNA. /FEA=mRNA /GEN |
| 218312_s_at | 1448.4 | 1058.5 | -1.37 | gb:N1023926.1 /DEF=Homo sapiens hypothetical protein FLJ12895 (FLJ12895), mRNA. /FEA=mRNA /GEN |
| 208942_s_at | 1752.5 | 1285 | -1.36 | Consensus Includes gb:BE866511 /FEA=EST /DB_XREF=gi:10315287 /DB_XREF=est:60167885F1 /CLON |
| 205694_at | 8659.9 | 6373.5 | -1.36 | gb:N1000550.1 /DEF=Homo sapiens tyrosinase-related protein 1 (TYRP1), mRNA. /FEA=mRNA /GEN=TY |
| 218502_s_at | 869.2 | 643.3 | -1.35 | gb:N1014112.1 /DEF=Homo sapiens trichorhinophalangeal syndrome I gene (TRPS1), mRNA. /FEA=mRNA |
| 212149_at | 1181.2 | 873.3 | -1.35 | Consensus includes gb:AW470003 /FEA=EST /DB_XREF=gi:7040109 /DB_XREF=est:qr27f05.x1 /CLONE=I |
| 44563_at | 1890.1 | 1396.1 | -1.35 | Cluster Incl. A1858000:wj69b05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2408049 /clone_end=3 /gb= |
| 222339_x_at | 1090.7 | 813.7 | -1.34 | Consensus includes gb:A1054381 /FEA=EST /DB_XREF=gi:3322168 /DB_XREF=est:qi64d09.x1 /CLONE=IM |
| 203455_s_at | 4309.5 | 3206.2 | -1.34 | gb:N1002970.1 /DEF=Homo sapiens spermidinase N1-acetyltransferase (SAT), mRNA. /FEA=mRNA /GEN=PRKY /P |
| 208279_at | 1172.2 | 879.7 | -1.33 | gb:N1002760.1 /DEF=Homo sapiens protein kinase, Y-linked (PRKY), mRNA. /FEA=mRNA /GEN=PRKY /P |
| 209293_x_at | 1191.3 | 894.8 | -1.33 | gb:U16153.1 /DEF=Human Id-4H protein mRNA, complete cds. /FEA=mRNA /PROD=Id-4H protein /DB_XRE |
| 219489_s_at | 1288.2 | 972.4 | -1.32 | gb:N101782.1 /DEF=Homo sapiens hypothetical protein FLJ20435 (FLJ20435), mRNA. /FEA=mRNA /GE |
| 201588_at | 1377.6 | 1039.7 | -1.32 | gb:N1004786.1 /DEF=Homo sapiens thioredoxin-like, 32kD (TXNL), mRNA. /FEA=mRNA /GEN=TXNL /PR |
| 221478_at | 2075.5 | 1569 | -1.32 | Consensus Includes gb:AL132665.1 /DEF=Homo sapiens mRNA; cDNA DKFZp566E034 (from clone DKFZ |
| 222230_s_at | 1182.9 | 902.9 | -1.31 | Consensus includes gb:AK022248.1 /DEF=Homo sapiens cDNA FLJ12186 fls, clone MAMMA1000824, wea |
| 201143_s_at | 1045.1 | 802.7 | -1.3 | gb:BC002513.1 /DEF=Homo sapiens, eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kD), clo |
| 217731_s_at | 4498.4 | 3453.3 | -1.3 | gb:N1021999.1 /DEF=Homo sapiens Integral membrane protein 2B (ITM2B), mRNA. /FEA=mRNA /GEN=IT |
| 203445_s_at | 1260.4 | 980.1 | -1.29 | gb:N1005730.1 /DEF=Homo sapiens conserved gene amplified in osteosarcoma (OS4), mRNA. /FEA=mR |
| 214041_x_at | 1480.3 | 1159.4 | -1.28 | Consensus includes gb:BE857772 /FEA=EST /DB_XREF=gi:10372131 /DB_XREF=est:7d62a11.x1 /CLONE= |
| 218456_at | 1508.6 | 1180.2 | -1.28 | gb:N1023925.1 /DEF=Homo sapiens hypothetical protein FLJ22569 (FLJ22569), mRNA. /FEA=mRNA /GE |
| 201860_s_at | 1531.3 | 1195 | -1.28 | gb:N100930.1 /DEF=Homo sapiens plasminogen activator, tissue (PLAT), mRNA. /FEA=mRNA /GEN=PL |
| 211740_at | 959.7 | 758.1 | -1.27 | gb:BC005922.1 /DEF=Homo sapiens, Similar to islet cell autoantigen 1 (69kD), clone MGC:14523, mRNA, c |
| 38447_at | 1331.4 | 1049.4 | -1.27 | Cluster Incl. U08438:Human beta-adrenergic receptor kinase (ADRBK1) gene /cgs=(40,2109) /gb=U08438 /g |
| 202379_s_at | 1646.6 | 1298.2 | -1.27 | Consensus includes gb:U92706 /DEF=Human rearranged immunoglobulin heavy chain (A1VH3) gene, par |
| 216557_x_at | 866.4 | 686.8 | -1.26 | Consensus includes gb:X96588.1 /DEF=H.sapiens mRNA for H-RYK receptor tyrosine kinase. /FEA=mRNA |
| 216976_s_at | 884.9 | 703.7 | -1.26 | Consensus includes gb:X96588.1 /DEF=H.sapiens mRNA for H-RYK receptor tyrosine kinase. /FEA=mRNA |
| 209108_at | 890.7 | 709 | -1.26 | gb:AF053453.1 /DEF=Homo sapiens tetraspan TM4SF (TSPAN-6) mRNA, complete cds. /FEA=mRNA /GEN |
| 202732_at | 1565.6 | 1241.8 | -1.26 | gb:N1007066.1 /DEF=Homo sapiens protein kinase (cAMP-dependent, catalytic) inhibitor gamma (PKIG) |
| 213064_at | 1259.4 | 1008.1 | -1.25 | Consensus Includes gb:N64802 /FEA=EST /DB_XREF=gi:1212631 /DB_XREF=est:yz31b05.s1 /CLONE=IMA |
| 201345_s_at | 1290 | 1033.1 | -1.25 | gb:N1003339.1 /DEF=Homo sapiens ubiquitin-conjugating enzyme E2D 2 (homologous to yeast UBC45) |
| 217958_at | 1316 | 1053.4 | -1.25 | gb:N1016146.1 /DEF=Homo sapiens PTD009 protein (PTD009), mRNA. /FEA=mRNA /GEN=PTD009 /PROD |
| 207804_s_at | 1429.3 | 1144.2 | -1.25 | gb:N1004108.1 /DEF=Homo sapiens ficolin (collagenfibrinogen domain-containing lectin) 2 (hucolin) (FC |

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|-----------------|--------|--------|-------|--|
| 221392_at | 704.8 | 567.7 | -1.24 | gb:NM_016944.1 /DEF=Homo sapiens taste receptor, type 2, member 4 (TAS2R4), mRNA. /FEA=CDS /GEN |
| 202371_at | 1322.2 | 1070.3 | -1.24 | gb:NM_024863.1 /DEF=Homo sapiens hypothetical protein FLJ21174 (FLJ21174), mRNA. /FEA=mRNA /GE |
| 209028_s_at | 1330.1 | 1075.1 | -1.24 | gb:AF006516.1 /DEF=Homo sapiens eps8 binding protein e3B1 mRNA, complete cds. /FEA=mRNA /PROD |
| 201163_s_at | 2634.1 | 2120.6 | -1.24 | gb:NM_001553.1 /DEF=Homo sapiens insulin-like growth factor binding protein 7 (IGFBP7), mRNA. /FEA= |
| 217094_s_at | 833.3 | 679.9 | -1.23 | Consensus includes gb:AL109923 /DEF=Human DNA sequence from clone RP3-468O1 on chromosome 2 |
| 221975_s_at | 1251.9 | 1018.5 | -1.23 | Consensus includes gb:AL1539305 /FEA=EST /DB_XREF=gi:4453440 /DB_XREF=est:te50h12.x1 /CLONE=IM |
| 201885_s_at | 1491.4 | 1216.3 | -1.23 | gb:NM_000398.3 /DEF=Homo sapiens diaphorase (NADH) (cytochrome b-5 reductase) (DIA1), nuclear gen |
| 201358_s_at | 4906.6 | 4002.2 | -1.23 | gb:NM_016451.1 /DEF=Homo sapiens coatomer protein complex, subunit beta (COPB), mRNA. /FEA=mRN |
| 205255_x_at | 1084.3 | 887.1 | -1.22 | gb:NM_003202.1 /DEF=Homo sapiens transcription factor 7 (T-cell specific, HMG-box) (TCF7), mRNA. /FE |
| AFFX-hum_alu_at | 8222.3 | 6745.5 | -1.22 | U14573 Human Alu-Sq subfamily consensus sequence. |
| 205647_at | 939.1 | 773.3 | -1.21 | gb:NM_002879.1 /DEF=Homo sapiens RAD52 (S. cerevisiae) homolog (RAD52), mRNA. /FEA=mRNA /GEN= |
| 212932_at | 975.3 | 806 | -1.21 | Consensus includes gb:AK022494.1 /DEF=Homo sapiens cDNA FLJ12432 fis, clone NT2RM1000018, highl |
| 44617_at | 1273.4 | 1048.3 | -1.21 | Cluster Incl. AL431902:ti26e07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2131620 /clone_end=3 /gb=A |
| 202001_s_at | 1383.4 | 1146.6 | -1.21 | gb:NM_002490.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (14kD, B |
| 210704_at | 1701.2 | 1404.6 | -1.21 | gb:L17328.1 /DEF=Human pre-TNK cell associated protein (3Ci) mRNA, complete cds. /FEA=mRNA /GEN= |
| 214892_x_at | 1087.8 | 908.1 | -1.2 | Consensus includes gb:BC004262.1 /DEF=Homo sapiens, Similar to cactin, clone IMAGE:3609158, mRNA |
| 211458_s_at | 2696.4 | 2244.7 | -1.2 | gb:AF180519.1 /DEF=Homo sapiens GABA-A receptor-associated protein mRNA, complete cds. /FEA=mR |
| 209787_s_at | 944.3 | 1135.1 | 1.2 | gb:BC001282.1 /DEF=Homo sapiens, high-mobility group (nonhistone chromosomal) protein 17-like 3, clo |
| 203067_at | 978.7 | 1170.7 | 1.2 | gb:NM_003477.1 /DEF=Homo sapiens Pyruvate dehydrogenase complex, lipoyl-containing component X; |
| 221607_x_at | 1542.4 | 1844.7 | 1.2 | gb:BC001920.1 /DEF=Homo sapiens, actin, gamma 1, clone MGC:3728, mRNA, complete cds. /FEA=mRNA |
| 200749_at | 1558.5 | 1877.4 | 1.2 | Consensus includes gb:BF112006 /FEA=EST /DB_XREF=gi:10941619 /DB_XREF=est:7137e05.x1 /CLONE= |
| 210563_x_at | 728.4 | 881.3 | 1.21 | gb:U97075.1 /DEF=Homo sapiens FLICE-like inhibitory protein short form mRNA, complete cds. /FEA=mR |
| 210652_s_at | 930.7 | 1128.2 | 1.21 | gb:BC004399.1 /DEF=Homo sapiens, clone MGC:10985, mRNA, complete cds. /FEA=mRNA /PROD=Unkno |
| 205711_x_at | 933.2 | 1127.7 | 1.21 | gb:NM_005174.1 /DEF=Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, gamma |
| 202609_at | 1008.3 | 1216 | 1.21 | gb:NM_004447.1 /DEF=Homo sapiens epidermal growth factor receptor pathway substrate 8 (EPS8), mRN |
| 203887_s_at | 1184.7 | 1432 | 1.21 | gb:NM_000361.1 /DEF=Homo sapiens thrombomodulin (THBD), mRNA. /FEA=mRNA /GEN=THBD /PROD= |
| 203011_at | 1198.1 | 1447.7 | 1.21 | gb:NM_005536.2 /DEF=Homo sapiens inositol(myo)-1(or 4)-monophosphatase 1 (IMPA1), mRNA. /FEA=mR |
| 208808_s_at | 1218.8 | 1471.5 | 1.21 | gb:BC000903.1 /DEF=Homo sapiens, high-mobility group (nonhistone chromosomal) protein 2, clone MGC |
| 212297_at | 1232.1 | 1488.3 | 1.21 | Consensus includes gb:BF218804 /FEA=EST /DB_XREF=gi:11112494 /DB_XREF=est:601882315F1 /CLON |
| 202090_s_at | 1265.9 | 1529.2 | 1.21 | gb:NM_006830.1 /DEF=Homo sapiens ubiquinol-cytochrome c reductase (6.4kD) subunit (UQCRC), mRNA. |
| 208274_at | 1279.6 | 1546.8 | 1.21 | gb:NM_022375.1 /DEF=Homo sapiens oculomedin (OCLM), mRNA. /FEA=mRNA /GEN=OCLM /PROD=ocul |
| 218388_at | 795.9 | 968.5 | 1.22 | gb:NM_012088.1 /DEF=Homo sapiens 6-phosphogluconolactonase (PGLS), mRNA. /FEA=mRNA /GEN=PG |
| 202034_x_at | 879.2 | 1073.3 | 1.22 | gb:NM_014781.1 /DEF=Homo sapiens KIAA0203 gene product (KIAA0203), mRNA. /FEA=mRNA /GEN=KIA |
| 219771_at | 914.2 | 1116.3 | 1.22 | gb:NM_017752.1 /DEF=Homo sapiens hypothetical protein FLJ20298 (FLJ20298), mRNA. /FEA=mRNA /GE |
| 212774_at | 974.8 | 1190.7 | 1.22 | Consensus includes gb:AJ223321 /DEF=Homo sapiens RP58 gene, complete CDS /FEA=mRNA /DB_XREF |

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|-------------|--------|--------|------|---|
| 211929_at | 1445.7 | 1763.9 | 1.22 | Consensus includes gb:AA527502 /FEA=EST /DB_XREF=gi:2269571 /DB_XREF=est:ng41f10.s1 /CLONE=I |
| 214022_s_at | 1771.3 | 2152.7 | 1.22 | Consensus includes gb:AA749101 /FEA=EST /DB_XREF=gi:2789059 /DB_XREF=est:ny11d02.s1 /CLONE= |
| 213588_x_at | 2240 | 2734.2 | 1.22 | Consensus includes gb:AA838274 /FEA=EST /DB_XREF=gi:2913073 /DB_XREF=est:oe90c01.s1 /CLONE= |
| 203480_s_at | 1138.4 | 1396 | 1.23 | gb:NM_014928.1 /DEF=Homo sapiens KIAA1046 protein (KIAA1046), mRNA. /FEA=mRNA /GEN=KIAA1046 |
| 209921_at | 1381.1 | 1693.9 | 1.23 | gb:AB040875.1 /DEF=Homo sapiens hxCt mRNA for cystineglutamate exchanger, complete cds. /FEA=m |
| 209067_s_at | 1481.5 | 1826.3 | 1.23 | gb:DB9092.1 /DEF=Homo sapiens hnrnp JKTBP mRNA, complete cds. /FEA=mRNA /GEN=hnrnp JKTBP |
| 208768_x_at | 1771 | 2185.9 | 1.23 | gb:D17652.1 /DEF=Human mRNA for HBP15L22, complete cds. /FEA=mRNA /PROD=HBP15L22 /DB_XREF |
| 208881_x_at | 876.9 | 1088.7 | 1.24 | gb:BC005247.1 /DEF=Homo sapiens, isopentenyl-diphosphate delta isomerase, clone MGC:12281, mRNA, |
| 204440_at | 1161.4 | 1436.5 | 1.24 | gb:NM_004233.1 /DEF=Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfam |
| 201217_x_at | 1202.9 | 1491.9 | 1.24 | gb:NM_000967.1 /DEF=Homo sapiens ribosomal protein L3 (RPL3), mRNA. /FEA=mRNA /GEN=RPL3 /PRO |
| 205849_s_at | 1456.4 | 1812.5 | 1.24 | gb:NM_006294.1 /DEF=Homo sapiens ubiquinol-cytochrome c reductase binding protein (UQCRB), mRNA |
| 216526_x_at | 1847 | 2282 | 1.24 | Consensus includes gb:AK024836.1 /DEF=Homo sapiens cDNA: FLJ21183 fis, clone CAS11634, highly sir |
| 217848_s_at | 2233.8 | 2766 | 1.24 | gb:NM_021129.1 /DEF=Homo sapiens pyrophosphatase (inorganic) (PP), nuclear gene encoding mitochon |
| 217127_at | 766.9 | 961.3 | 1.25 | Consensus includes gb:AL354872 /DEF=Human DNA sequence from clone RP11-42O15 on chromosome |
| 201843_s_at | 862.9 | 1082.6 | 1.25 | gb:NM_004105.2 /DEF=Homo sapiens EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1), |
| 213583_x_at | 1342.8 | 1674.6 | 1.25 | Consensus includes gb:BE964125 /FEA=EST /DB_XREF=gi:11767593 /DB_XREF=est:601657809R1 /CLON |
| 209277_at | 1483.8 | 1861.3 | 1.25 | Consensus includes gb:AL574096 /FEA=EST /DB_XREF=gi:12933969 /DB_XREF=est:AL574096 /CLONE=C |
| 203935_at | 753.7 | 949.3 | 1.26 | gb:NM_001105.2 /DEF=Homo sapiens activin A receptor, type I (ACVR1), mRNA. /FEA=mRNA /GEN=ACVR |
| 35201_at | 790.6 | 995.7 | 1.26 | Cluster Incl. X16135:Human mRNA for novel heterogeneous nuclear RNP protein, L protein /cds=(28,1704 |
| 219805_at | 971.7 | 1225.3 | 1.26 | gb:NM_022101.1 /DEF=Homo sapiens hypothetical protein FLJ22965 (FLJ22965), mRNA. /FEA=mRNA /GE |
| 203753_at | 988.9 | 1247.5 | 1.26 | gb:NM_003199.1 /DEF=Homo sapiens transcription factor 4 (TCF4), mRNA. /FEA=mRNA /GEN=TCF4 /PRO |
| 212183_at | 1149.4 | 1448.6 | 1.26 | Consensus includes gb:AW511135 /FEA=EST /DB_XREF=gi:7149213 /DB_XREF=est:hd43g08.x1 /CLONE= |
| 201772_at | 717.2 | 909.2 | 1.27 | gb:NM_015878.1 /DEF=Homo sapiens antizyme inhibitor (LOC51582), mRNA. /FEA=mRNA /GEN=LOC5158 |
| 218864_at | 767.1 | 976.2 | 1.27 | gb:AF116610.1 /DEF=Homo sapiens PRO0929 mRNA, complete cds. /FEA=mRNA /PROD=PRO0929 /DB_X |
| 213300_at | 797.7 | 1010.6 | 1.27 | Consensus includes gb:AW168132 /FEA=EST /DB_XREF=gi:6399657 /DB_XREF=est:yg60c11.x1 /CLONE= |
| 218350_s_at | 850.7 | 1082.9 | 1.27 | gb:NM_015895.1 /DEF=Homo sapiens geminin (LOC51053), mRNA. /FEA=mRNA /GEN=LOC51053 /PROD= |
| 210689_at | 928.6 | 1177.7 | 1.27 | gb:AF314090.1 /DEF=Homo sapiens claudin 14 (CLDN14) mRNA, complete cds. /FEA=mRNA /GEN=CLDN1 |
| 201215_at | 987.9 | 1255.9 | 1.27 | gb:NM_005032.2 /DEF=Homo sapiens plastin 3 (T isoform) (PLS3), mRNA. /FEA=mRNA /GEN=PLS3 /PROD |
| 213961_s_at | 995.1 | 1265.1 | 1.27 | Consensus includes gb:A077556 /FEA=EST /DB_XREF=gi:3411964 /DB_XREF=est:oz33f08.x1 /CLONE=IM |
| 213009_s_at | 722 | 924.8 | 1.28 | Consensus includes gb:AK022701.1 /DEF=Homo sapiens cDNA FLJ12639 fis, clone NT2RM4001938, highl |
| 218171_at | 757.5 | 966.8 | 1.28 | gb:AF195514.1 /DEF=Homo sapiens VPS4-2 ATPase (VPS42) mRNA, complete cds. /FEA=mRNA /GEN=VP |
| 202194_at | 881 | 1129.6 | 1.28 | Consensus includes gb:AL117354 /DEF=Human DNA sequence from clone RP5-976O13 on chromosome |
| 213712_at | 963.2 | 1232.1 | 1.28 | Consensus includes gb:BF508639 /FEA=EST /DB_XREF=gi:11591937 /DB_XREF=est:UI-H-BI4-aop-a-07-0- |
| 204685_s_at | 969.3 | 1240.6 | 1.28 | Consensus includes gb:R52647 /FEA=EST /DB_XREF=gi:814549 /DB_XREF=est:y82f05.s1 /CLONE=IMAG |
| 208020_s_at | 1161.5 | 1483.2 | 1.28 | gb:NM_000719.1 /DEF=Homo sapiens calcium channel, voltage-dependent, L type, alpha 1C subunit (CAC |

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|-------------|--------|--------|------|--|
| 200043_at | 1271.2 | 1625.4 | 1.28 | gb:NM_004450.1 /DEF=Homo sapiens enhancer of rudimentary (Drosophila) homolog (ERH), mRNA. /FEA= |
| 211983_x_at | 1944.2 | 2494 | 1.28 | Consensus includes gb:BE741683 /FEA=EST /DB_XREF=gi:10155675 /DB_XREF=est:601594740F1 /CLON |
| 210303_at | 694 | 897.4 | 1.29 | gb:AF262032.1 /DEF=Homo sapiens MAB21L2 protein (MAB21L2), mRNA, complete cds. /FEA=mRNA /GEN |
| 204135_at | 770.6 | 990.5 | 1.29 | gb:NM_014890.1 /DEF=Homo sapiens downregulated in ovarian cancer 1 (DOC1), mRNA. /FEA=mRNA /GEN |
| 208939_at | 836.2 | 1078.1 | 1.29 | Consensus includes gb:AV682679 /FEA=EST /DB_XREF=gi:10284542 /DB_XREF=est:AV682679 /CLONE=G |
| 222112_at | 971.6 | 1254.1 | 1.29 | Consensus includes gb:AV710549 /FEA=EST /DB_XREF=gi:10729178 /DB_XREF=est:AV710549 /CLONE=C |
| 201761_at | 995.2 | 1288 | 1.29 | gb:NM_006636.2 /DEF=Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), met |
| 209927_s_at | 1033.5 | 1333.5 | 1.29 | gb:AF261137.1 /DEF=Homo sapiens HT031 mRNA, complete cds. /FEA=mRNA /PROD=HT031 /DB_XREF= |
| 200994_at | 1110.6 | 1433.5 | 1.29 | Consensus includes gb:BG291787 /FEA=EST /DB_XREF=gi:13050002 /DB_XREF=est:602386007F1 /CLON |
| 201553_s_at | 1743.8 | 2251.4 | 1.29 | gb:NM_005561.2 /DEF=Homo sapiens lysosomal-associated membrane protein 1 (LAMP1), mRNA. /FEA=m |
| 202842_s_at | 1969.5 | 2544.2 | 1.29 | gb:AL080081.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564F1862 (from clone DKFZp564F1862); comple |
| 208625_s_at | 673.9 | 874.4 | 1.3 | gb:AF104913.1 /DEF=Homo sapiens eukaryotic protein synthesis initiation factor mRNA, complete cds. /F |
| 208652_at | 735.5 | 958.3 | 1.3 | gb:BC000400.1 /DEF=Homo sapiens, protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform |
| 202657_s_at | 784.2 | 1017.9 | 1.3 | gb:NM_014755.1 /DEF=Homo sapiens KIAA0127 gene product (KIAA0127), mRNA. /FEA=mRNA /GEN=KIA |
| 220439_at | 862.9 | 1120.9 | 1.3 | gb:NM_024892.1 /DEF=Homo sapiens hypothetical protein FLJ11700 (FLJ11700), mRNA. /FEA=mRNA /GE |
| 203613_s_at | 1029.9 | 1340.6 | 1.3 | gb:NM_002493.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (17kD, B1 |
| 208870_x_at | 1134.7 | 1474.8 | 1.3 | gb:BC000931.2 /DEF=Homo sapiens, ATP synthase, H+ transporting, mitochondrial F1 complex, gamma p |
| 222297_x_at | 2003.5 | 2598.8 | 1.3 | Consensus includes gb:AV738806 /FEA=EST /DB_XREF=gi:10856387 /DB_XREF=est:AV738806 /CLONE=C |
| 201891_s_at | 4410.8 | 5746.1 | 1.3 | gb:NM_004048.1 /DEF=Homo sapiens beta-2-microglobulin (B2M), mRNA. /FEA=mRNA /GEN=B2M /PROD |
| 200733_s_at | 829.2 | 1087.4 | 1.31 | gb:U48296.1 /DEF=Homo sapiens protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA, comple |
| 221471_at | 857 | 1126.7 | 1.31 | Consensus includes gb:AW173623 /FEA=EST /DB_XREF=gi:6439571 /DB_XREF=est:xj10a08.x1 /CLONE=I |
| 215691_x_at | 984.1 | 1289.6 | 1.31 | Consensus includes gb:AV702994 /FEA=EST /DB_XREF=gi:10719324 /DB_XREF=est:AV702994 /CLONE=A |
| 219410_at | 816.3 | 1078.8 | 1.32 | gb:NM_018004.1 /DEF=Homo sapiens hypothetical protein FLJ10134 (FLJ10134), mRNA. /FEA=mRNA /GE |
| 201128_s_at | 855.5 | 1130 | 1.32 | gb:NM_001096.1 /DEF=Homo sapiens ATP citrate lyase (ACLY), mRNA. /FEA=mRNA /GEN=ACLY /PROD= |
| 218283_at | 1072.4 | 1416 | 1.32 | gb:NM_016305.1 /DEF=Homo sapiens kiasa-iso protein (LOC51188), mRNA. /FEA=mRNA /GEN=LOC51188 / |
| 213134_x_at | 1205.3 | 1588.8 | 1.32 | Consensus includes gb:AK026491.1 /DEF=Homo sapiens cDNA: FLJ22838 fls, clone KAIA4494, highly sim |
| 200088_x_at | 1304.4 | 1718.3 | 1.32 | gb:AY009128.1 /DEF=Homo sapiens ISCU2 (ISCU) mRNA, complete cds, alternatively spliced. /FEA=mRN |
| 209075_s_at | 1315.1 | 1739.3 | 1.32 | gb:NM_005923.2 /DEF=Homo sapiens mitogen-activated protein kinase kinase kinase 5 (MAP3K5), mRNA. |
| 203837_at | 789.8 | 1050.4 | 1.33 | gb:NM_000194.1 /DEF=Homo sapiens hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrom |
| 202854_at | 890.1 | 1183.4 | 1.33 | gb:NM_014977.1 /DEF=Homo sapiens KIAA0670 proteinacinus (KIAA0670), mRNA. /FEA=mRNA /GEN=KIA |
| 201715_s_at | 959 | 1274.8 | 1.33 | gb:NM_022977.1 /DEF=Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4), transcript varia |
| 202422_s_at | 1001.6 | 1331.2 | 1.33 | gb:NM_003543.2 /DEF=Homo sapiens H4 histone family, member H (H4FH), mRNA. /FEA=mRNA /GEN=H4 |
| 208180_s_at | 633.7 | 846.9 | 1.34 | Consensus includes gb:AW194730 /FEA=EST /DB_XREF=gi:6473630 /DB_XREF=est:xn43d11.x1 /CLONE= |
| 202693_s_at | 653.4 | 878.3 | 1.34 | gb:AF130054.1 /DEF=Homo sapiens clone FLB4816 PRO1252 mRNA, complete cds. /FEA=mRNA /PROD=P |
| 211452_x_at | 735.8 | 987.9 | 1.34 | |

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|-------------|---------|--------|------|--|
| 205655_at | 752 | 1009.9 | 1.34 | gb:NM_002393.1 /DEF=Homo sapiens mouse double minute 4, human homolog of; p53-binding protein (M |
| 200761_s_at | 1063.1 | 1421.5 | 1.34 | gb:NM_006407.2 /DEF=Homo sapiens vitamin A responsive; cytoskeleton related (JWA), mRNA. /FEA=mR |
| 210933_s_at | 575.7 | 780 | 1.35 | gb:BC004908.1 /DEF=Homo sapiens, clone MGC:4655, mRNA, complete cds. /FEA=mRNA /PROD=Unknown |
| 217052_x_at | 887.9 | 1203.1 | 1.35 | Consensus includes gb:AK024108.1 /DEF=Homo sapiens cDNA FLJ14046 fis, clone HEMBA1006461. /FEA |
| 209186_at | 948.5 | 1280.1 | 1.35 | gb:M23114.1 /DEF=Homo sapiens calcium-ATPase (HK1) mRNA, complete cds. /FEA=mRNA /GEN=HK1 /D |
| 200027_at | 966 | 1308 | 1.35 | gb:NM_004539.2 /DEF=Homo sapiens asparaginyl-tRNA synthetase (NARS), mRNA. /FEA=mRNA /GEN=NA |
| 200602_at | 1390.8 | 1884.5 | 1.35 | gb:NM_000484.1 /DEF=Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer di |
| 209089_at | 1726.1 | 2328 | 1.35 | gb:BC001267.1 /DEF=Homo sapiens, RAB5A, member RAS oncogene family, clone MGC:5048, mRNA, con |
| 202032_s_at | 762.8 | 1038.7 | 1.36 | gb:NM_006122.1 /DEF=Homo sapiens mannosidase, alpha, class 2A, member 2 (MAN2A2), mRNA. /FEA=m |
| 222209_s_at | 825.7 | 1125 | 1.36 | Consensus includes gb:AK000684.1 /DEF=Homo sapiens cDNA FLJ20677 fis, clone KAIA4183. /FEA=mRN |
| 208073_x_at | 835.1 | 1139.7 | 1.36 | gb:NM_003316.1 /DEF=Homo sapiens tetratricopeptide repeat domain 3 (TTC3), mRNA. /FEA=mRNA /GEN |
| 202324_s_at | 1253.9 | 1711.4 | 1.36 | gb:NM_022735.1 /DEF=Homo sapiens golgi resident protein GCP60 (GCP60), mRNA. /FEA=mRNA /GEN |
| 200958_s_at | 1545.1 | 2094.3 | 1.36 | gb:NM_005625.1 /DEF=Homo sapiens syndecan binding protein (syntenin) (SDCBP), mRNA. /FEA=mRNA /GEN=G |
| 200092_s_at | 1710.3 | 2332.8 | 1.36 | Consensus includes gb:BF216701 /FEA=EST /DB_XREF=gi:11110287 /DB_XREF=est:601884615F1 /CLON |
| 220978_at | 670.3 | 918.9 | 1.37 | gb:NM_030966.1 /DEF=Homo sapiens keratin associated protein 1.3 (KRTAP1.3), mRNA. /FEA=mRNA /GE |
| 200694_s_at | 947.1 | 1294.2 | 1.37 | gb:NM_020414.2 /DEF=Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box polypeptide 24 (DDX24), mRNA. |
| 207507_s_at | 1006.1 | 1378.2 | 1.37 | gb:NM_001689.1 /DEF=Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit |
| 50314_i_at | 1007.9 | 1380.1 | 1.37 | Cluster Incl. A1761506:wi61b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394717 /clone_end=3 /gb= |
| 214327_x_at | 4489.1 | 6143.6 | 1.37 | Consensus includes gb:AI888178 /FEA=EST /DB_XREF=gi:5593342 /DB_XREF=est:wm40b09.x1 /CLONE= |
| 210528_at | 655.3 | 905.7 | 1.38 | gb:AF010447.1 /DEF=Homo sapiens MHC class I related protein 1 isoform C (MR1C) mRNA, complete cds |
| 218445_at | 749 | 1031.5 | 1.38 | gb:NM_018649.1 /DEF=Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA. /FEA=mRNA /GE |
| 209022_at | 915 | 1265.6 | 1.38 | Consensus includes gb:AK026678.1 /DEF=Homo sapiens, ribosomal protein S17, clone MGC:11144, mRNA, highly sim |
| 211487_x_at | 1100.2 | 1521.5 | 1.38 | gb:BC004886.1 /DEF=Homo sapiens, ribosomal protein S17, clone MGC:11144, mRNA, complete cds. /FE |
| 201662_s_at | 1105.8 | 1520.7 | 1.38 | gb:D89053.1 /DEF=Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds. /FEA=mRNA /PROD=A |
| 205788_s_at | 1152.8 | 1590 | 1.38 | gb:NM_014827.1 /DEF=Homo sapiens KIAA0663 gene product (KIAA0663), mRNA. /FEA=mRNA /GEN=KIA |
| 213857_s_at | 1317.6 | 1824 | 1.38 | Consensus includes gb:BG230614 /FEA=EST /DB_XREF=gi:12725656 /DB_XREF=est:naf41b12.x1 /CLONE |
| 217883_at | 661.1 | 919.4 | 1.39 | gb:NM_015702.1 /DEF=Homo sapiens hypothetical protein (CL25022), mRNA. /FEA=mRNA /GEN=CL25022 |
| 214972_at | 812.9 | 1129.6 | 1.39 | Consensus includes gb:AU144791 /FEA=EST /DB_XREF=gi:11006312 /DB_XREF=est:AU144791 /CLONE= |
| 206133_at | 835 | 1160.1 | 1.39 | gb:NM_017523.1 /DEF=Homo sapiens XIAP associated factor-1 (IRS1), mRNA. /FEA=mRNA /GEN=H |
| 204686_at | 845.7 | 1174.6 | 1.39 | gb:NM_005544.1 /DEF=Homo sapiens insulin receptor substrate 1 (IRS1), mRNA. /FEA=mRNA /GEN=IRS1 |
| 208855_s_at | 1361.2 | 1886.8 | 1.39 | gb:AF083420.1 /DEF=Homo sapiens brain-specific STE20-like protein kinase 3 (STK3) mRNA, complete cd |
| 212852_s_at | 1406.7 | 1957.7 | 1.39 | Consensus includes gb:AL538601 /FEA=EST /DB_XREF=gi:12867040 /DB_XREF=est:AL538601 /CLONE=C |
| 209122_at | 2259 | 3138.9 | 1.39 | gb:BC005127.1 /DEF=Homo sapiens, adipose differentiation-related protein, clone MGC:10598, mRNA, con |
| 212869_x_at | 11100.7 | 15395 | 1.39 | Consensus includes gb:AI721229 /FEA=EST /DB_XREF=gi:5038485 /DB_XREF=est:as68c10.x1 /CLONE=IM |
| 212588_at | 793.9 | 1113.1 | 1.4 | Consensus includes gb:Y00062.1 /DEF=Human mRNA for T200 leukocyte common antigen (CD45, LC-A). |

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|-------------|--------|--------|------|---|
| 204681_s_at | 864.4 | 1212.5 | 1.4 | gb:NM_012294.1 /DEF=Homo sapiens guanine nucleotide exchange factor for Rap1; M-Ras-regulated GEF |
| 217741_s_at | 947.8 | 1323.2 | 1.4 | Consensus includes gb:AW471220 /FEA=EST /DB_XREF=gi:7041326 /DB_XREF=est:xv13g08.x1 /CLONE= |
| 201071_x_at | 1080.1 | 1508.7 | 1.4 | gb:NM_012433.1 /DEF=Homo sapiens splicing factor 3b, subunit 1, 155kD (SF3B1), mRNA. /FEA=mRNA /G |
| 202391_at | 1231 | 1729.4 | 1.4 | gb:NM_006317.1 /DEF=Homo sapiens brain acid-soluble protein 1 (BASP1), mRNA. /FEA=mRNA /GEN=BA |
| 221773_at | 1257.6 | 1764.6 | 1.4 | Consensus includes gb:AW575374 /FEA=EST /DB_XREF=gi:7246913 /DB_XREF=est:U1-HF-BL0-adc-c-12-0 |
| 219077_s_at | 798.1 | 1124.8 | 1.41 | gb:NM_016373.1 /DEF=Homo sapiens WW domain-containing oxidoreductase (WWOX), mRNA. /FEA=mRN |
| 201975_at | 801.1 | 1126 | 1.41 | gb:NM_002956.1 /DEF=Homo sapiens retin (Reed-Steinberg cell-expressed intermediate filament-associa |
| 212974_at | 803.9 | 1134.2 | 1.41 | Consensus includes gb:A1808958 /FEA=EST /DB_XREF=gi:5395524 /DB_XREF=est:wf67a09.x1 /CLONE=IM |
| 209541_at | 680.8 | 969.5 | 1.42 | Consensus includes gb:A1972496 /FEA=EST /DB_XREF=gi:5769242 /DB_XREF=est:wr38c02.x1 /CLONE=IM |
| 221626_at | 705.8 | 1004.6 | 1.42 | gb:AL136548.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761G18121 (from clone DKFZp761G18121); com |
| 217845_x_at | 1154.5 | 1638.6 | 1.42 | gb:NM_014056.1 /DEF=Homo sapiens DKFZP564K247 protein (DKFZP564K247), mRNA. /FEA=mRNA /GEN |
| 200014_s_at | 531.4 | 760.4 | 1.43 | gb:NM_004500.1 /DEF=Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1C2) (HNRPC), mRNA |
| 213102_at | 1053 | 1504.3 | 1.43 | Consensus includes gb:Z78330 /FEA=EST /DB_XREF=gi:1495103 /DB_XREF=est:HSZ78330 /CLONE=2.49 |
| 201366_at | 1159.1 | 1658.7 | 1.43 | gb:NM_004034.1 /DEF=Homo sapiens annexin A7 (ANXA7), transcript variant 2, mRNA. /FEA=mRNA /GEN |
| 200077_s_at | 1274.2 | 1826 | 1.43 | gb:D87914.1 /DEF=Human mRNA for ornithine decarboxylase antizyme, complete cds. /FEA=mRNA /GEN= |
| 200834_s_at | 1443.2 | 2062.6 | 1.43 | gb:NM_001024.1 /DEF=Homo sapiens mRNA for ornithine decarboxylase antizyme, complete cds. /FEA=mRNA /GEN= |
| 216342_x_at | 1948.4 | 2782.9 | 1.43 | Consensus includes gb:AL121916 /DEF=Human DNA sequence from clone RP1-189G13 on chromosome |
| 214003_x_at | 5953.6 | 8516 | 1.43 | Consensus includes gb:BF184532 /FEA=EST /DB_XREF=gi:11062829 /DB_XREF=est:601842837F1 /CLON |
| 203080_s_at | 697.8 | 1007.4 | 1.44 | gb:NM_013450.1 /DEF=Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA. |
| 203423_at | 855.1 | 1230.5 | 1.44 | gb:NM_002899.2 /DEF=Homo sapiens retinol-binding protein 1, cellular (RBP1), mRNA. /FEA=mRNA /GEN |
| 213037_x_at | 1158.4 | 1670.4 | 1.44 | Consensus includes gb:AJ132258.1 /DEF=Homo sapiens mRNA for staufen protein, partial. /FEA=mRNA / |
| 208724_s_at | 1261.5 | 1811.2 | 1.44 | gb:BC000905.1 /DEF=Homo sapiens, RAB1, member RAS oncogene family, clone MGC:5233, mRNA, com |
| 218213_s_at | 1344.3 | 1940.3 | 1.44 | gb:NM_014206.1 /DEF=Homo sapiens chromosome 11 open reading frame 10 (C11orf10), mRNA. /FEA=mR |
| 208691_at | 1660.6 | 2397.6 | 1.44 | gb:BC001188.1 /DEF=Homo sapiens, transferrin receptor (p90, CD71), clone MGC:3151, mRNA, complete c |
| 211509_s_at | 2270.4 | 3279 | 1.44 | gb:AB015639.1 /DEF=Homo sapiens ASY mRNA, complete cds. /FEA=mRNA /GEN=ASY /DB_XREF=gi:582 |
| 210705_s_at | 669.4 | 970.2 | 1.45 | gb:AF220028.1 /DEF=Homo sapiens tripartite motif protein TRIM5 isoform delta (TRIM5) mRNA, complete |
| 213017_at | 1002.2 | 1450.4 | 1.45 | Consensus includes gb:AL534702 /FEA=EST /DB_XREF=gi:12798195 /DB_XREF=est:AL534702 /CLONE=C |
| 211073_x_at | 1324.5 | 1923.8 | 1.45 | gb:BC006483.1 /DEF=Homo sapiens, ribosomal protein L3, clone MGC:4393, mRNA, complete cds. /FEA= |
| 200627_at | 726.7 | 1061.7 | 1.46 | gb:BC003005.1 /DEF=Homo sapiens, unactive progesterone receptor, 23 kD, clone MGC:4004, mRNA, com |
| 207854_at | 834.6 | 1221.6 | 1.46 | gb:NM_002102.1 /DEF=Homo sapiens, glycoprotein E (GYPE), mRNA. /FEA=mRNA /GEN=GYPE /PROD=gly |
| 206424_at | 1073.3 | 1564.3 | 1.46 | gb:NM_000783.1 /DEF=Homo sapiens cytochrome P450, subfamily XXVIA, polypeptide 1 (CYP26A1), mRN |
| 221775_x_at | 1363.1 | 1995.8 | 1.46 | Consensus includes gb:BG152979 /FEA=EST /DB_XREF=gi:12665009 /DB_XREF=est:nah24c06.y1 /CLONE |
| 41220_at | 1497.5 | 2189.4 | 1.46 | Cluster Incl. AB023208: Homo sapiens mRNA for KIAA0991 protein, complete cds /cds=(732,2000) /gb=AB0 |
| 204595_s_at | 1546.3 | 2261.5 | 1.46 | Consensus includes gb:A1300520 /FEA=EST /DB_XREF=gi:3959866 /DB_XREF=est:qn55e06.x1 /CLONE=IM |
| 205434_s_at | 619 | 912.6 | 1.47 | Consensus includes gb:AW451954 /FEA=EST /DB_XREF=gi:6992730 /DB_XREF=est:U1-H-BI3-alt-h-06-0-U |

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|-------------|--------|--------|------|--|
| 213960_at | 821.4 | 1205 | 1.47 | Consensus Includes gb:T87225 /FEA=EST /DB_XREF=gi:715577 /DB_XREF=est:yc81f06.s1 /CLONE=IMAG |
| 200738_s_at | 897 | 1315.1 | 1.47 | gb:NM_000291.1 /DEF=Homo sapiens phosphoglycerate kinase 1 (PGK1), mRNA. /FEA=mRNA /GEN=PGK |
| 36888_at | 976.5 | 1435.6 | 1.47 | Cluster Incl. AB020648:Homo sapiens mRNA for KIAA0841 protein, partial cds /cds={0,1925} /gb=AB02064 |
| 203752_s_at | 1192.4 | 1752.8 | 1.47 | gb:NM_005354.2 /DEF=Homo sapiens Jun D proto-oncogene (JUND), mRNA. /FEA=mRNA /GEN=JUND /PR |
| 218007_s_at | 1237.8 | 1821.1 | 1.47 | gb:NM_015920.1 /DEF=Homo sapiens 40S ribosomal protein S27 isoform (LOC51065), mRNA. /FEA=mRNA |
| 214211_at | 2495.1 | 3657.2 | 1.47 | Consensus Includes gb:AA083483 /FEA=EST /DB_XREF=gi:1625544 /DB_XREF=est:zn32a06.s1 /CLONE=I |
| 206087_x_at | 860.4 | 1273.6 | 1.48 | gb:NM_000410.1 /DEF=Homo sapiens hemochromatosis (HFE), mRNA. /FEA=mRNA /GEN=HFE /PROD=he |
| 203725_at | 929.5 | 1374.6 | 1.48 | gb:NM_001924.2 /DEF=Homo sapiens growth arrest and DNA-damage-inducible, alpha (GADD45A), mRNA |
| 207473_at | 995.2 | 1472.9 | 1.48 | gb:NM_002418.1 /DEF=Homo sapiens motilin (MLN), mRNA. /FEA=mRNA /GEN=MLN /PROD=motilin /DB |
| 210095_s_at | 1213.3 | 1793.5 | 1.48 | gb:M31159.1 /DEF=Human growth hormone-dependent insulin-like growth factor-binding protein mRNA, c |
| 219454_at | 1241.7 | 1836.1 | 1.48 | gb:NM_015507.2 /DEF=Homo sapiens EGF-like domain, multiple 6 (EGFL6), mRNA. /FEA=mRNA /GEN=EG |
| 201606_s_at | 555 | 827.5 | 1.49 | Consensus Includes gb:BE796924 /FEA=EST /DB_XREF=gi:10218031 /DB_XREF=est:601587284F1 /CLON |
| 211149_at | 592.5 | 882.3 | 1.49 | gb:AF000994.1 /DEF=Homo sapiens ubiquitously expressed TPR motif, Y isoform (UTY) mRNA, alternative transcript 3 |
| 219803_at | 745.2 | 1109.9 | 1.49 | gb:NM_014495.1 /DEF=Homo sapiens angiotensin-like 3 (ANGPTL3), mRNA. /FEA=mRNA /GEN=ANGPTL |
| 213864_s_at | 1371.3 | 2043.5 | 1.49 | Consensus Includes gb:AI985751 /FEA=EST /DB_XREF=gi:5813028 /DB_XREF=est:wr76h07.x1 /CLONE=IM |
| 202029_x_at | 2695.6 | 4029.9 | 1.49 | gb:NM_000999.1 /DEF=Homo sapiens ribosomal protein L38 (RPL38), mRNA. /FEA=mRNA /GEN=RPL38 /P |
| 212006_at | 722.4 | 1080.4 | 1.5 | Consensus Includes gb:AU149908 /FEA=EST /DB_XREF=gi:11011429 /DB_XREF=est:AU149908 /CLONE= |
| 211207_s_at | 907.1 | 1364.7 | 1.5 | gb:AF129166.1 /DEF=Homo sapiens long-chain acyl-CoA synthetase 5 (LACS5) mRNA, complete cds. /FE |
| 202690_s_at | 941.3 | 1412.2 | 1.5 | gb:BC001721.1 /DEF=Homo sapiens, small nuclear ribonucleoprotein D1 polypeptide (16kD), clone MGC:2 |
| 201012_at | 1121.9 | 1687.5 | 1.5 | gb:NM_000700.1 /DEF=Homo sapiens annexin A1 (ANXA1), mRNA. /FEA=mRNA /GEN=ANXA1 /PROD=ann |
| 208616_s_at | 1476.4 | 2219.6 | 1.5 | gb:U48297.1 /DEF=Homo sapiens protein tyrosine phosphatase PTPCAAX2 (hPTPCAAX2) mRNA, comple |
| 214672_at | 617.9 | 936 | 1.51 | Consensus Includes gb:AB023215.1 /DEF=Homo sapiens mRNA for KIAA0998 protein, partial cds. /FEA=m |
| 207458_at | 837.1 | 1267.7 | 1.51 | gb:NM_024035.1 /DEF=Homo sapiens hypothetical protein MGC3113 (MGC3113), mRNA. /FEA=mRNA /GE |
| 218226_s_at | 890 | 1341.4 | 1.51 | gb:NM_004547.2 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4 (15kD, B1 |
| 200004_at | 668.4 | 1018.2 | 1.52 | gb:NM_001418.1 /DEF=Homo sapiens eukaryotic translation initiation factor 4 gamma, 2 (EIF4G2), mRNA. |
| 204470_at | 877.6 | 1336.7 | 1.52 | gb:NM_001511.1 /DEF=Homo sapiens GRO1 oncogene (melanoma growth stimulating activity, alpha) (GR |
| 214179_s_at | 951.6 | 1445.2 | 1.52 | Consensus Includes gb:H93013 /FEA=EST /DB_XREF=gi:1099341 /DB_XREF=est:yv07g07.s1 /CLONE=IMA |
| 200912_s_at | 1002.7 | 1526.1 | 1.52 | gb:NM_001967.2 /DEF=Homo sapiens eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2), mRNA |
| 213214_x_at | 1289.6 | 1963.7 | 1.52 | Consensus Includes gb:AW190090 /FEA=EST /DB_XREF=gi:6464570 /DB_XREF=est:x159a03.x1 /CLONE=I |
| 210592_s_at | 1939.2 | 2944.8 | 1.52 | gb:M55580.1 /DEF=Human spermidinase N1-acetyltransferase mRNA, complete cds. /FEA=mRNA / |
| 209123_at | 670.4 | 1023.3 | 1.53 | gb:BC000576.1 /DEF=Homo sapiens, quinald dihydropteridine reductase, clone MGC:1657, mRNA, comple |
| 201059_at | 855.2 | 1305 | 1.53 | gb:NM_005231.1 /DEF=Homo sapiens ems1 sequence (mammary tumor and squamous cell carcinoma-as |
| 210779_x_at | 879.7 | 1342.9 | 1.53 | gb:AB037701.1 /DEF=Homo sapiens SIP1-beta mRNA for SMN Interacting protein1-beta, complete cds. /F |
| 222108_at | 1647 | 2512 | 1.53 | Consensus Includes gb:AC004010 /DEF=Human BAC clone GS1-99H8 /FEA=CDS /DB_XREF=gi:2781385 / |
| 221748_s_at | 3191.3 | 4867.2 | 1.53 | Consensus Includes gb:AL046979 /FEA=EST /DB_XREF=gi:5435035 /DB_XREF=est:DKFZp586K0617_s1 / |

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|-------------|--------|--------|------|--|
| 203738_at | 605.8 | 933 | 1.54 | Consensus includes gb:A1421192 /FEA=EST /DB_XREF=gi:4267123 /DB_XREF=est:tf24e12.x1 /CLONE=IM |
| 202289_s_at | 820.2 | 1265.2 | 1.54 | gb:NM_006997.1 /DEF=Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), mRNA |
| 221368_at | 1184.2 | 1823.4 | 1.54 | gb:NM_005383.1 /DEF=Homo sapiens slalidase 2 (cytosolic slalidase) (NEU2), mRNA. /FEA=CDS /GEN=NE |
| 212687_at | 1312.1 | 2022.2 | 1.54 | Consensus includes gb:AL110164.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586i0324 (from clone DKFZ |
| 207720_at | 829.2 | 1287 | 1.55 | gb:NM_000427.1 /DEF=Homo sapiens loridin (LOR), mRNA. /FEA=mRNA /GEN=LOR /PROD=loridin /DB_ |
| 213151_s_at | 1012.7 | 1568 | 1.55 | Consensus includes gb:AU157515 /FEA=EST /DB_XREF=gi:11019036 /DB_XREF=est:AU157515 /CLONE= |
| 201429_s_at | 8390.7 | 13018 | 1.55 | gb:NM_000998.1 /DEF=Homo sapiens ribosomal protein L37a (RPL37A), mRNA. /FEA=mRNA /GEN=RPL37 |
| 221505_at | 713 | 1109 | 1.56 | Consensus includes gb:AW612574 /FEA=EST /DB_XREF=gi:7317760 /DB_XREF=est:hh05b12.x1 /CLONE= |
| 206050_s_at | 923.2 | 1436.2 | 1.56 | gb:NM_002939.1 /DEF=Homo sapiens ribonucleaseangiogenin inhibitor (RNH), mRNA. /FEA=mRNA /GEN= |
| 201352_at | 1668.1 | 2597.9 | 1.56 | gb:NM_014263.1 /DEF=Homo sapiens YME1 (S.cerevisiae)-like 1 (YME1L1), mRNA. /FEA=mRNA /GEN=YM |
| 207574_s_at | 1693.8 | 2663.8 | 1.57 | gb:NM_015675.1 /DEF=Homo sapiens growth arrest and DNA-damage-inducible, beta (GADD45B), mRNA. |
| 201502_s_at | 1752.1 | 2766.1 | 1.58 | Consensus includes gb:A1078167 /FEA=EST /DB_XREF=gi:3412575 /DB_XREF=est:oz30d08.x1 /CLONE=IM |
| 203324_s_at | 1021.4 | 1622.2 | 1.59 | gb:NM_001233.1 /DEF=Homo sapiens caveolin 2 (CAV2), mRNA. /FEA=mRNA /GEN=CAV2 /PROD=caveoli |
| 201922_at | 1151.5 | 1828.4 | 1.59 | gb:NM_014886.1 /DEF=Homo sapiens hypothetical protein (YR-29), mRNA. /FEA=mRNA /GEN=YR-29 /PRO |
| 200662_s_at | 1207.9 | 1919.1 | 1.59 | gb:NM_014765.1 /DEF=Homo sapiens translocase of outer mitochondrial membrane 20 (yeast) homolog (K |
| 202786_at | 590 | 942 | 1.6 | gb:NM_013233.1 /DEF=Homo sapiens Ste-20 related kinase (SPAK), mRNA. /FEA=mRNA /GEN=SPAK /PRO |
| 211946_s_at | 1057.1 | 1696.4 | 1.6 | Consensus includes gb:AL096857.1 /DEF=Novel human mRNA from chromosome 1, which has similaritie |
| 212230_at | 2196.1 | 3509.5 | 1.6 | Consensus includes gb:AV725664 /FEA=EST /DB_XREF=gi:10831279 /DB_XREF=est:AV725664 /CLONE=H |
| 209397_at | 551.4 | 887.6 | 1.61 | gb:BC000147.1 /DEF=Homo sapiens, Similar to malic enzyme 2, NAD(+)-dependent, mitochondrial, clone M |
| 206157_at | 770.3 | 1239.3 | 1.61 | gb:NM_002852.1 /DEF=Homo sapiens pentaxin-related gene, rapidly induced by IL-1 beta (PTX3), mRNA. |
| 65635_at | 922.6 | 1482.8 | 1.61 | Cluster Incl. AL044097:DKFZp434M1928_s1 Homo sapiens cDNA, 3' end /clone=DKFZp434M1928 /clone_e |
| 220044_x_at | 947.8 | 1523.4 | 1.61 | gb:NM_016424.1 /DEF=Homo sapiens cisplatin resistance-associated overexpressed protein (LUC7A), mR |
| 213347_x_at | 4440.7 | 7156.5 | 1.61 | Consensus includes gb:AW132023 /FEA=EST /DB_XREF=gi:6133630 /DB_XREF=est:xe71b05.x1 /CLONE= |
| 212386_at | 695.8 | 1127.6 | 1.62 | Consensus includes gb:BF592782 /FEA=EST /DB_XREF=gi:11685106 /DB_XREF=est:7J94d06.x1 /CLONE= |
| 222229_x_at | 887.8 | 1438.1 | 1.62 | Consensus includes gb:AL121871 /DEF=Human DNA sequence from clone RP13-258O15 on chromosome |
| 211628_x_at | 1306.8 | 2116.7 | 1.62 | gb:J04755.1 /DEF=Human ferritin H processed pseudogene, complete cds. /FEA=mRNA /GEN=FTHP1 /DB |
| 200718_s_at | 2433.8 | 3951.9 | 1.62 | Consensus includes gb:AA927664 /FEA=EST /DB_XREF=gi:3076484 /DB_XREF=est:om71h10.s1 /CLONE= |
| 200891_s_at | 1070.4 | 1748.9 | 1.63 | gb:NM_003144.2 /DEF=Homo sapiens signal sequence receptor, alpha (translocon-associated protein alph |
| 200840_at | 1103.4 | 1796.6 | 1.63 | gb:NM_005548.1 /DEF=Homo sapiens lysyl-tRNA synthetase (KARS), mRNA. /FEA=mRNA /GEN=KARS /PR |
| 200026_at | 2436.3 | 3981.2 | 1.63 | gb:NM_000995.1 /DEF=Homo sapiens ribosomal protein L34 (RPL34), mRNA. /FEA=mRNA /GEN=RPL34 /P |
| 203621_at | 788.3 | 1292.2 | 1.64 | gb:NM_002492.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (16kD, SG |
| 201665_x_at | 1237.2 | 2026.2 | 1.64 | gb:NM_001021.1 /DEF=Homo sapiens ribosomal protein S17 (RPS17), mRNA. /FEA=mRNA /GEN=RPS17 /P |
| 200069_at | 761.1 | 1255.9 | 1.65 | Consensus includes gb:AI656011 /FEA=EST /DB_XREF=gi:4739990 /DB_XREF=est:tt42e08.x1 /CLONE=IM |
| 208645_s_at | 857.6 | 1418.9 | 1.65 | gb:AF116710.1 /DEF=Homo sapiens PRO2640 mRNA, complete cds. /FEA=mRNA /PROD=PRO2640 /DB_X |
| 207594_s_at | 584.1 | 967.9 | 1.66 | gb:NM_003895.1 /DEF=Homo sapiens synaptotagmin 1 (SYNJ1), mRNA. /FEA=mRNA /GEN=SYNJ1 /PROD=s |

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|-------------|--------|--------|------|---|
| 207268_x_at | 800 | 1335.2 | 1.67 | gb:NM_005759.1 /DEF=Homo sapiens abi-interactor 12 (SH3-containing protein) (AIP-1), mRNA. /FEA=mR |
| 212426_s_at | 1040.3 | 1747.8 | 1.68 | Consensus includes gb:BF033313 /FEA=EST /DB_XREF=gi:10741025 /DB_XREF=est:601458002F1 /CLON |
| 213020_at | 687.8 | 1164.2 | 1.69 | Consensus includes gb:A1814252 /FEA=EST /DB_XREF=gi:5425467 /DB_XREF=est:wj70g04.x1 /CLONE=IM |
| 221301_at | 883.1 | 1492.6 | 1.69 | gb:NM_025258.1 /DEF=Homo sapiens NG37 protein (G7C), mRNA. /FEA=CDS /GEN=G7C /PROD=NG37 pro |
| 201738_at | 1818.7 | 3115.5 | 1.71 | gb:NM_005875.1 /DEF=Homo sapiens translation factor su1 homolog (GC20), mRNA. /FEA=mRNA /GEN= |
| 208780_x_at | 989.6 | 1703.7 | 1.72 | gb:AF154847.1 /DEF=Homo sapiens 33 kDa Vamp-associated protein (VAMP) mRNA, complete cds. /FEA= |
| 200963_x_at | 2844.6 | 4902.4 | 1.72 | gb:NM_000993.1 /DEF=Homo sapiens ribosomal protein L31 (RPL31), mRNA. /FEA=mRNA /GEN=RPL31 /P |
| 201166_s_at | 609.4 | 1056 | 1.73 | gb:NM_014676.1 /DEF=Homo sapiens pumilio (Drosophila) homolog 1 (PUM1), mRNA. /FEA=mRNA /GEN= |
| 215127_s_at | 859.7 | 1484.5 | 1.73 | Consensus includes gb:AL517946 /FEA=EST /DB_XREF=gi:12781439 /DB_XREF=est:AL517946 /CLONE=C |
| 200817_x_at | 1151.7 | 1992.4 | 1.73 | gb:NM_001014.1 /DEF=Homo sapiens ribosomal protein S10 (RPS10), mRNA. /FEA=mRNA /GEN=RPS10 /P |
| 208394_x_at | 1022.8 | 1780.2 | 1.74 | gb:NM_007036.2 /DEF=Homo sapiens endothelial cell-specific molecule 1 (ESM1), mRNA. /FEA=mRNA /GE |
| 200765_x_at | 813.6 | 1420.1 | 1.75 | gb:NM_001903.1 /DEF=Homo sapiens catenin (cadherin-associated protein) 1 (CTNNA1), m |
| 208671_at | 1071.4 | 1872.8 | 1.75 | gb:AF164794.1 /DEF=Homo sapiens caspase-like apoptosis regulatory protein 2 (clarp) mRNA, alternative |
| 209939_x_at | 937 | 1654.1 | 1.77 | gb:AF005775.1 /DEF=Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit |
| 202325_s_at | 1089.2 | 1925.1 | 1.77 | gb:NM_001685.1 /DEF=Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit |
| 201599_at | 1162.8 | 2062.9 | 1.77 | gb:NM_000274.1 /DEF=Homo sapiens ornithine aminotransferase (gyrate atrophy) (OAT), nuclear gene en |
| 200726_at | 1060.9 | 1890.6 | 1.78 | gb:NM_002710.1 /DEF=Homo sapiens protein phosphatase 1, catalytic subunit, gamma isoform (PPP1CC) |
| 204271_s_at | 1388.4 | 2482.4 | 1.79 | gb:M74921.1 /DEF=Human endothelin receptor mRNA, complete cds. /FEA=mRNA /GEN=ETs /PROD=endo |
| 201061_s_at | 980.1 | 1762.8 | 1.8 | gb:M81635.1 /DEF=Homo sapiens erythrocyte membrane protein mRNA, complete cds. /FEA=mRNA /GEN |
| 213356_x_at | 1607.4 | 2895.7 | 1.8 | Consensus includes gb:AL568186 /FEA=EST /DB_XREF=gi:12922280 /DB_XREF=est:AL568186 /CLONE=C |
| 217720_at | 939.3 | 1699.8 | 1.81 | gb:NM_016139.1 /DEF=Homo sapiens 16.7Kd protein (LOC51142), mRNA. /FEA=mRNA /GEN=LOC51142 /P |
| 211072_x_at | 1034 | 1875.4 | 1.81 | gb:BC006481.1 /DEF=Homo sapiens, tubulin alpha 1, clone MGC:4387, mRNA, complete cds. /FEA=mRNA |
| 218319_at | 1401.8 | 2535.9 | 1.81 | gb:NM_020651.2 /DEF=Homo sapiens pellino (Drosophila) homolog 1 (PELI1), mRNA. /FEA=mRNA /GEN= |
| 213165_at | 470.8 | 856.1 | 1.82 | Consensus includes gb:A1041204 /FEA=EST /DB_XREF=gi:3280398 /DB_XREF=est:ov77g06.x1 /CLONE=IM |
| 202466_at | 796.9 | 1458.3 | 1.83 | gb:NM_006999.2 /DEF=Homo sapiens topoisomerase-related function protein 4-1 (TRF4), mRNA. /FEA=m |
| 208864_s_at | 1284.6 | 2369.3 | 1.84 | gb:AF313911.1 /DEF=Homo sapiens thioredoxin mRNA, complete cds. /FEA=mRNA /PROD=thioredoxin /D |
| 204744_s_at | 796.2 | 1475.9 | 1.85 | gb:NM_013417.1 /DEF=Homo sapiens isoleucine-tRNA synthetase (IARS), transcript variant long, mRNA. |
| 210512_s_at | 1309 | 2425.1 | 1.85 | gb:AF022375.1 /DEF=Homo sapiens vascular endothelial growth factor mRNA, complete cds. /FEA=mRNA |
| 205003_at | 521.8 | 971.5 | 1.86 | gb:NM_014705.1 /DEF=Homo sapiens KIAA0716 gene product (KIAA0716), mRNA. /FEA=mRNA /GEN=KIA |
| 201492_s_at | 4873 | 9066.3 | 1.86 | gb:NM_021104.1 /DEF=Homo sapiens ribosomal protein L41 (RPL41), mRNA. /FEA=mRNA /GEN=RPL41 /P |
| 212814_at | 812.3 | 1527.1 | 1.88 | Consensus includes gb:AB020635.1 /DEF=Homo sapiens mRNA for KIAA0828 protein, partial cds. /FEA=m |
| 214039_s_at | 826.1 | 1553.8 | 1.88 | Consensus includes gb:T15777 /FEA=EST /DB_XREF=gi:517939 /DB_XREF=est:IB1875 /UG=Hs.296398 Ho |
| 213320_at | 372.6 | 705.6 | 1.89 | Consensus includes gb:AL551971 /FEA=EST /DB_XREF=gi:12890422 /DB_XREF=est:AL551971 /CLONE=C |
| 211945_s_at | 1121.2 | 2114.1 | 1.89 | Consensus includes gb:BG500301 /FEA=EST /DB_XREF=gi:13461818 /DB_XREF=est:602546969F1 /CLON |
| 212391_x_at | 862.9 | 1637.2 | 1.9 | Consensus includes gb:A1925635 /FEA=EST /DB_XREF=gi:5661686 /DB_XREF=est:wo34f07.x1 /CLONE=IM |

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|-------------|--------|---------|------|--|
| 219293_s_at | 1063.7 | 2030.4 | 1.91 | gb:NM_013341.1 /DEF=Homo sapiens hypothetical protein (PTD004), mRNA. /FEA=mRNA /GEN=PTD004 /P |
| 202130_at | 1103.9 | 2110 | 1.91 | Consensus includes gb:AA725102 /FEA=EST /DB_XREF=gi:2742809 /DB_XREF=est:ai08h05.s1 /CLONE=1 |
| 201667_at | 1642.1 | 3142.6 | 1.91 | gb:NM_000165.2 /DEF=Homo sapiens gap junction protein, alpha 1, 43kD (connexin 43) (GJA1), mRNA. /F |
| 208905_at | 1692.1 | 3248.8 | 1.92 | gb:BC005299.1 /DEF=Homo sapiens, cytochrome c, clone MGC:12367, mRNA, complete cds. /FEA=mRNA |
| 200926_at | 2997.9 | 5750.3 | 1.92 | gb:NM_001025.1 /DEF=Homo sapiens ribosomal protein S23 (RPS23), mRNA. /FEA=mRNA /GEN=RPS23 /P |
| 202644_s_at | 900.9 | 1735.9 | 1.93 | gb:NM_006290.1 /DEF=Homo sapiens tumor necrosis factor, alpha-induced protein 3 (TNFAIP3), mRNA. / |
| 212788_x_at | 1074.3 | 2077.9 | 1.93 | Consensus includes gb:BG537190 /FEA=EST /DB_XREF=gi:13528922 /DB_XREF=est:602555589F1 /CLON |
| 211959_at | 3320.9 | 6398.2 | 1.93 | Consensus includes gb:AW007532 /FEA=EST /DB_XREF=gi:5856310 /DB_XREF=est:ws52h07.x1 /CLONE= |
| 200063_s_at | 1186.6 | 2305.7 | 1.94 | gb:BC002398.1 /DEF=Homo sapiens, nucleophosmin (nucleolar phosphoprotein B23, numatrin), clone MG |
| 200061_s_at | 1051.5 | 2055.2 | 1.95 | gb:BC000523.1 /DEF=Homo sapiens, Similar to ribosomal protein S24, clone MGC:8595, mRNA, complete |
| 217824_at | 647.7 | 1283.7 | 1.98 | Consensus includes gb:AW500009 /FEA=EST /DB_XREF=gi:7112213 /DB_XREF=est:UI-HF-BN0-aki-e-09-0 |
| 201842_s_at | 1026 | 2041 | 1.99 | Consensus includes gb:A1826799 /FEA=EST /DB_XREF=gi:5447470 /DB_XREF=est:wk56d07.x1 /CLONE=I |
| 201266_at | 1298.5 | 2599 | 2 | gb:NM_003330.1 /DEF=Homo sapiens thioredoxin reductase 1 (TXNRD1), mRNA. /FEA=mRNA /PROD=riboso |
| 200062_s_at | 1489.1 | 2983.5 | 2 | gb:L05095.1 /DEF=Homo sapiens ribosomal protein L30 mRNA, complete cds. /FEA=mRNA /GEN=RPL7 /PRO |
| 200717_x_at | 1676.7 | 3349 | 2 | gb:NM_000971.1 /DEF=Homo sapiens ribosomal protein L7 (RPL7), mRNA. /FEA=mRNA /GEN=RPL7 /PRO |
| 203414_at | 765.7 | 1536.2 | 2.01 | gb:NM_012329.1 /DEF=Homo sapiens monocyte to macrophage differentiation-associated (MMD), mRNA. |
| 208896_at | 496.3 | 1011.5 | 2.04 | Consensus includes gb:X98743.1 /DEF=H.sapiens mRNA for RNA helicase (Myc-regulated dead box prote |
| 208635_x_at | 1804.2 | 3674.5 | 2.04 | Consensus includes gb:BF976260 /FEA=EST /DB_XREF=gi:12343475 /DB_XREF=est:602245139F1 /CLON |
| 212185_x_at | 1875.1 | 3822.5 | 2.04 | Consensus includes gb:NM_005953.1 /DEF=Homo sapiens metallothionein 2A (MT2A), mRNA. /FEA=CDS |
| 200735_x_at | 1773.5 | 3635.4 | 2.05 | gb:NM_005594.1 /DEF=Homo sapiens nascent-polypeptide-associated complex alpha polypeptide (NACA |
| 212578_x_at | 769 | 1581.2 | 2.06 | Consensus includes gb:BF026595 /FEA=EST /DB_XREF=gi:10734307 /DB_XREF=est:601672736F1 /CLON |
| 213084_x_at | 5532.5 | 11421.8 | 2.06 | Consensus includes gb:BF125158 /FEA=EST /DB_XREF=gi:10964198 /DB_XREF=est:601762392F1 /CLON |
| 55065_at | 799.2 | 1655.1 | 2.07 | Cluster Incl. AL120554:DKFZp761B169_s1 Homo sapiens cDNA, 3' end /clone=DKFZp761B169 /clone_end |
| 220960_x_at | 1047.8 | 2166.4 | 2.07 | gb:NM_000983.1 /DEF=Homo sapiens ribosomal protein L22 (RPL22), mRNA. /FEA=mRNA /GEN=RPL22 /P |
| 201994_at | 1398 | 2887 | 2.07 | gb:NM_012286.1 /DEF=Homo sapiens MORF-related gene X (KIAA0026), mRNA. /FEA=mRNA /GEN=KIAA0 |
| 202592_s_at | 536.8 | 1126.6 | 2.1 | gb:NM_014233.1 /DEF=Homo sapiens upstream binding protein mRNA, complete cds. /FEA=mRNA / |
| 209066_x_at | 1107.6 | 2328.6 | 2.1 | gb:M26700.1 /DEF=Human mitochondrial ubiquinone-binding protein mRNA, complete cds. /FEA=mRNA / |
| 200095_x_at | 2342.5 | 4908.5 | 2.1 | Consensus includes gb:AA320764 /FEA=EST /DB_XREF=gi:1973113 /DB_XREF=est:EST23183 /UG=Hs.76 |
| 201064_s_at | 568.3 | 1198.8 | 2.11 | gb:NM_003819.2 /DEF=Homo sapiens poly(A)-binding protein, cytoplasmic 4 (Inducible form) (PABPC4), m |
| 201031_s_at | 477.7 | 1015.3 | 2.13 | gb:NM_005520.1 /DEF=Homo sapiens heterogeneous nuclear ribonucleoprotein H1 (H) (HNRPH1), mRNA. |
| 213478_at | 595.6 | 1278.9 | 2.15 | Consensus includes gb:AB028949.1 /DEF=Homo sapiens mRNA for KIAA1026 protein, partial cds. /FEA=m |
| 202347_s_at | 507.3 | 1100.8 | 2.17 | gb:AB022435.1 /DEF=Homo sapiens LIG mRNA for E2 ubiquitin-conjugating enzyme, complete cds. /FEA |
| 217739_s_at | 929.6 | 2042.9 | 2.2 | gb:NM_005746.1 /DEF=Homo sapiens pre-B-cell colony-enhancing factor (PBEF), mRNA. /FEA=mRNA /GE |
| 200032_s_at | 1928.9 | 4380.1 | 2.27 | gb:NM_000661.1 /DEF=Homo sapiens ribosomal protein L9 (RPL9), mRNA. /FEA=mRNA /GEN=RPL9 /PRO |
| 203405_at | 581.2 | 1323.4 | 2.28 | gb:NM_003720.1 /DEF=Homo sapiens Down syndrome critical region gene 2 (DSCR2), mRNA. /FEA=mRNA |

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|-------------|--------|---------|------|---|
| 204108_at | 754.9 | 1721.3 | 2.28 | Consensus includes gb:AL031778 /DEF=Human DNA sequence from clone 34B21 on chromosome 6p12.1 |
| 207783_x_at | 4353.8 | 9942.1 | 2.28 | gb:Nm_017627.1 /DEF=Homo sapiens hypothetical protein FLJ20030 (FLJ20030), mRNA. /FEA=mRNA /GE |
| 204651_at | 555.9 | 1273.9 | 2.29 | Consensus includes gb:AW003022 /FEA=EST /DB_XREF=gi:5849860 /DB_XREF=est:wq61d03.x1 /CLONE= |
| 213477_x_at | 648.1 | 1484.2 | 2.29 | Consensus includes gb:AL515273 /FEA=EST /DB_XREF=gi:12778766 /DB_XREF=est:AL515273 /CLONE=C |
| 205061_s_at | 659.8 | 1540 | 2.33 | gb:Nm_005033.1 /DEF=Homo sapiens polymyositis scleroderma autoantigen 1 (75kD) (PMSCL1), mRNA. / |
| 217975_at | 800 | 1867.3 | 2.33 | gb:Nm_016303.1 /DEF=Homo sapiens pp21 homolog (LOC51186), mRNA. /FEA=mRNA /GEN=LOC51186 /P |
| 203282_at | 875.1 | 2042 | 2.33 | gb:Nm_000158.1 /DEF=Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzym |
| 208825_x_at | 5728.7 | 13420 | 2.34 | gb:U43701.1 /DEF=Human ribosomal protein L23a mRNA, complete cds. /FEA=mRNA /PROD=ribosomal p |
| 208834_x_at | 5712.9 | 13418.7 | 2.35 | gb:BC001865.1 /DEF=Homo sapiens, Similar to cadherin 1, type 1, E-cadherin (epithelial), clone MGC:1151 |
| 200893_at | 635.9 | 1516.9 | 2.39 | gb:Nm_004593.1 /DEF=Homo sapiens splicing factor, arginineserine-rich (transformer 2 Drosophila homo |
| 213101_s_at | 1221.2 | 3121 | 2.56 | Consensus includes gb:Z78330 /FEA=EST /DB_XREF=gi:1495103 /DB_XREF=est:HSZ78330 /CLONE=2.49 |
| 201257_x_at | 743.2 | 1916.6 | 2.58 | gb:Nm_001006.1 /DEF=Homo sapiens ribosomal protein S3A (RPS3A), mRNA. /FEA=mRNA /GEN=RPS3A |
| 221619_s_at | 1786.9 | 4643.6 | 2.6 | gb:AF189289.1 /DEF=Homo sapiens presenilin-associated protein mRNA, complete cds. /FEA=mRNA /PRO |
| 221474_at | 553.2 | 1487.2 | 2.69 | gb:U26162.1 /DEF=Human myosin regulatory light chain mRNA, complete cds. /FEA=mRNA /PROD=myos |
| 200933_x_at | 1461.7 | 4005.2 | 2.74 | gb:Nm_001007.1 /DEF=Homo sapiens ribosomal protein S4, X-linked (RPS4X), mRNA. /FEA=mRNA /GEN= |
| 212724_at | 623.7 | 1779.6 | 2.85 | Consensus includes gb:BG054844 /FEA=EST /DB_XREF=gi:12511973 /DB_XREF=est:nac90f11.x1 /CLONE |
| 209386_at | 1668.9 | 4862.3 | 2.91 | Consensus includes gb:AL346835 /FEA=EST /DB_XREF=gi:4084041 /DB_XREF=est:qp58g11.x1 /CLONE=IM |
| 216438_s_at | 1293 | 3817.8 | 2.95 | Consensus includes gb:AL133228 /DEF=Human DNA sequence from clone RP5-1071L10 on chromosome |
| 201406_at | 1612.2 | 4954 | 3.07 | gb:Nm_021029.1 /DEF=Homo sapiens ribosomal protein L44 (RPL44), mRNA. /FEA=mRNA /GEN=RPL44 /P |
| 201590_x_at | 855.9 | 2724.9 | 3.18 | gb:Nm_004039.1 /DEF=Homo sapiens annexin A2 (ANXA2), mRNA. /FEA=mRNA /GEN=ANXA2 /PROD=ann |
| 214938_x_at | 553.3 | 1774.2 | 3.21 | Consensus includes gb:AF283771.2 /DEF=Homo sapiens clone TCBAP0774 mRNA sequence. /FEA=mRNA |
| 201631_s_at | 1404.5 | 4524.6 | 3.22 | gb:Nm_003897.1 /DEF=Homo sapiens immediate early response 3 (IER3), mRNA. /FEA=mRNA /GEN=IER3 |
| 211185_s_at | 704 | 2311.5 | 3.28 | gb:AF130099.1 /DEF=Homo sapiens clone FLC1464 PRO3102 mRNA, complete cds. /FEA=mRNA /PROD=P |
| 204748_at | 1150 | 4628 | 4.02 | gb:Nm_000963.1 /DEF=Homo sapiens prostaglandin-endoperoxide synthase 2 (prostaglandin GH synthas |
| 205207_at | 2308.6 | 11218.4 | 4.86 | gb:Nm_000600.1 /DEF=Homo sapiens interleukin 6 (interferon, beta 2) (IL6), mRNA. /FEA=mRNA /GEN=IL6 |
| 211943_x_at | 2098.5 | 10217.5 | 4.87 | Consensus includes gb:AL565449 /FEA=EST /DB_XREF=gi:12916836 /DB_XREF=est:AL565449 /CLONE=C |